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184700

From: Whiteman, Brian
Sent: Monday, April 10, 2006 11:26 AM
To: STIC-Biotech/ChemLib
Subject: seq search

09816688 High et al.

SEQ ID NO: 1

- 1) commercial database
- 2) us patents and published us patent applications

Please limit search to 20 amino acids or less

Thank you,

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Remsen, 2D14
mail box 2C18
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

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Point of Contact:
Alexandra Wacławiw
Technical Info. Specialist
CH1 6402 Tel: 303-4491

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: 4/13
Date completed: 4/17
Searcher Prep Time: 10
Online Time: 11

Type of Search
NA# _____ AA# 1
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: 126 ✓
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____ ✓
WWW/Internet: _____
Other (Specify): _____

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OM protein - protein search, using sw model

Run on: April 13, 2006, 08:49:59 ; Search time 163 Seconds
(without alignments)
15.380 Million cell updates/sec

Title: US-09-816-688B-1

Perfect score: 30

Sequence: 1 RKRRKR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 389445

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	6	4	US-10-445-235-5
2	30	100.0	6	4	US-10-712-332-5
3	30	100.0	9	3	US-09-816-688A-1
4	30	100.0	15	5	US-10-912-764-45
5	27	90.0	8	3	US-09-876-904A-348
6	27	90.0	8	4	US-10-028-056-25
7	27	90.0	8	4	US-10-211-088-230
8	27	90.0	8	5	US-10-482-029-359
9	27	90.0	12	3	US-09-933-780C-35
10	27	90.0	13	3	US-09-746-170-39
11	27	90.0	19	4	US-10-225-567A-1183
12	27	90.0	21	3	US-09-864-761-48960
13	26	86.7	8	4	US-10-057-620-7
14	26	86.7	10	5	US-10-902-959-49
15	26	86.7	10	5	US-10-983-169-2
16	26	86.7	11	5	US-10-983-169-11
17	26	86.7	13	3	US-09-746-170-26
18	26	86.7	13	3	US-09-746-170-31
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103 24 80.0 8 3 US-09-847-946A-151
104 24 80.0 8 3 US-09-847-946A-157
105 24 80.0 8 3 US-09-876-904A-349
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148 24 80.0 9 3 US-09-847-946A-158
149 24 80.0 9 3 US-09-906-311C-13
150 24 80.0 9 4 US-10-083-960-5
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ALIGNMENTS

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RESULT 1
US-10-445-235-5
; Sequence 5, Application US/10445235
; Publication No. US20040005670A1
; GENERAL INFORMATION:
; APPLICANT: Katherine A. High
; APPLICANT: Rodney M. Camire
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT OF HEMOPHILIA A
; FILE REFERENCE: CHOP0176
; CURRENT APPLICATION NUMBER: US/10/445,235
; CURRENT FILING DATE: 2003-05-22
; PRIOR FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 6
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-445-235-5

Query Match 100.0%; Score 30; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRRKR 6
Db 1 RRRKR 6

RESULT 2
US-10-712-332-5
; Sequence 5, Application US/10712332
; Publication No. US20040072757A1
; GENERAL INFORMATION:
; APPLICANT: Wolf, David L.
; Sinha, Uma
; TITLE OF INVENTION: Agents Affecting Thrombosis and Hemostasis
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan, Lewis & Bockius LLP
; STREET: 1111 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/712,332
; FILING DATE: 13-Nov-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/671,346
; FILING DATE: 27-Sep-2000
; APPLICATION NUMBER: US 07/578,646
; FILING DATE: 1990-09-04
; APPLICATION NUMBER: US 07/808,329
; FILING DATE: 1991-12-16
; APPLICATION NUMBER: US 08/249,777
; FILING DATE: 1994-05-26
; APPLICATION NUMBER: US 08/268,003
; FILING DATE: 1994-06-29
; APPLICATION NUMBER: US 08/469,301
; FILING DATE: 1995-06-06
; APPLICATION NUMBER: US 09/016,403
; APPLICATION NUMBER: US 09/362,207
; FILING DATE: 1999-07-28
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael S. Tuscan, Ph.D.
; REGISTRATION NUMBER: 43,210
; REFERENCE/DOCKET NUMBER: 44481-5002-15-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 739-3000
; TELEFAX: (202) 739-3001
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-712-332-5

Query Match 100.0%; Score 30; DB 4; Length 6;
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Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRR 6
Db 1 RRRRR 6

RESULT 3

US-09-816-688A-1
; Sequence 1, Application US/09816688A
; Publication No. US20040102388A1
; GENERAL INFORMATION:
; APPLICANT: THE CHILDREN'S HOSPITAL OF PHILADELPHIA
; APPLICANT: HIGH, KATHERINE
; APPLICANT: MARGARITAS, PARIS
; APPLICANT: CAMRIE, RODNEY
; TITLE OF INVENTION: MODIFIED BLOOD CLOTTING FACTORS AND METHODS OF USE
; FILE REFERENCE: 018743-0278737
; CURRENT APPLICATION NUMBER: US/09/816,688A
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,331
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic proteolytic cleavage
; OTHER INFORMATION: peptide
US-09-816-688A-1

Query Match 100.0%; Score 30; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRR 6
Db 1 RRRRR 6

RESULT 4

US-10-912-764-45
; Sequence 45, Application US/10912764
; Publication No. US20050059122A1
; GENERAL INFORMATION:
; APPLICANT: SHEN, BEN
; TITLE OF INVENTION: TARGETED CARRIER FUSIONS FOR DELIVERY OF
; FILE REFERENCE: WARP:011US
; CURRENT APPLICATION NUMBER: US/10/912,764
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: 60/492,508
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-912-764-45

Query Match 100.0%; Score 30; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRR 6
Db 1 RRRRR 6

Db 5 RRRRR 10

RESULT 5

US-09-876-904A-348
; Sequence 348, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 348
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse Oct-2 protein transcription factors (Oct-2.1
; OTHER INFORMATION: for Oct-2.6 isoforms)
US-09-876-904A-348

Query Match 90.0%; Score 27; DB 3; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRR 6
Db 2 RRRRR 7

RESULT 6

US-10-028-056-25
; Sequence 25, Application US/10028056
; Publication No. US20020152483A1
; GENERAL INFORMATION:
; APPLICANT: REUE, KAREN
; APPLICANT: PTERFY, MIKLOS
; TITLE OF INVENTION: A NOVEL GENE ASSOCIATED WITH REGULATION OF ADIPOSITY AND INSULIN
; FILE REFERENCE: 407T-898010US
; CURRENT APPLICATION NUMBER: US/10/028,056
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 60/257,772
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-028-056-25

Query Match 90.0%; Score 27; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRR 6
Db 1 RRRRR 6

RESULT 7

US-10-211-088-230
; Sequence 230, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.

```
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular Bi
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 230
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Nuclear localization signal
US-10-211-088-230

Query Match          90.0%; Score 27; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRKR 6
Db 2 RRRRKR 7

RESULT 8
US-10-482-029-359
; Sequence 359, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 359
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-359

Query Match          90.0%; Score 27; DB 5; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRKR 6
Db 2 RRRRKR 7

RESULT 9
US-09-933-780C-35
; Sequence 35, Application US/09933780C
; Publication No. US20030229202A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMACEUTICALS INC.
; APPLICANT: GUO, Yong
; APPLICANT: MORSE, Clarence C
; APPLICANT: YAO, Zhengbin
; TITLE OF INVENTION: MEMBRANE PENETRATING PEPTIDES AND USES THEREOF
; FILE REFERENCE: HM2053 PCT
; CURRENT APPLICATION NUMBER: US/09/933,780C
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,647
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: GB 0103110.3
; PRIOR FILING DATE: 2001-02-07

; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular Bi
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 230
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Nuclear localization signal
US-10-211-088-230

Query Match          90.0%; Score 27; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRKR 6
Db 2 RRRRKR 7

RESULT 8
US-10-482-029-359
; Sequence 359, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 359
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-359

Query Match          90.0%; Score 27; DB 5; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRKR 6
Db 2 RRRRKR 7

RESULT 9
US-09-933-780C-35
; Sequence 35, Application US/09933780C
; Publication No. US20030229202A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMACEUTICALS INC.
; APPLICANT: GUO, Yong
; APPLICANT: MORSE, Clarence C
; APPLICANT: YAO, Zhengbin
; TITLE OF INVENTION: MEMBRANE PENETRATING PEPTIDES AND USES THEREOF
; FILE REFERENCE: HM2053 PCT
; CURRENT APPLICATION NUMBER: US/09/933,780C
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,647
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: GB 0103110.3
; PRIOR FILING DATE: 2001-02-07

; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular Bi
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
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; SEQ ID NO 230
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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Nuclear localization signal
US-10-211-088-230

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Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRKR 6
Db 2 RRRRKR 7

RESULT 10
US-09-746-170-39
; Sequence 39, Application US/09746170
; Patent No. US20020127543A1
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Walker, Stephen
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,804
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-746-170-39

Query Match          90.0%; Score 27; DB 3; Length 13;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRKR 6
Db 2 RRRRKR 7

RESULT 11
US-10-225-567A-1183
; Sequence 1183, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1183
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1183

Query Match          90.0%; Score 27; DB 4; Length 19;
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Best Local Similarity 83.3%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1;

QY 1 RKRRKR 6
|:|||||
Db 5 RRRKR 10

RESULT 12

US-09-864-761-48960

; Sequence 48960, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeonica-X-1

; CURRENT APPLICATION NUMBER: US/09/864, 761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 48960

; LENGTH: 21

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AC008171.1

; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.62

US-09-864-761-48960

Query Match 90.0%; Score 27; DB 3; Length 21;

Best Local Similarity 83.3%; Pred. No. 5.3e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1;

QY 1 RKRRKR 6
|:|||||
Db 10 RKRRR 15

RESULT 13

US-10-057-620-7

; Sequence 7, Application US/10057620

; Publication No. US20030229036A1

; GENERAL INFORMATION:

; APPLICANT: GENZYME CORPORATION

; APPLICANT: Scaria, Abraham

; APPLICANT: Wadsworth, Samuel C.

; TITLE OF INVENTION: METHODS FOR TREATING BLOOD COAGULATION DISORDERS

; FILE REFERENCE: 5046US

; CURRENT APPLICATION NUMBER: US/10/057,620

; CURRENT FILING DATE: 2001-10-25

; PRIOR APPLICATION NUMBER: PCT/US01/51391

; PRIOR FILING DATE: 2001-10-25

; PRIOR APPLICATION NUMBER: US 60/307,492

; PRIOR FILING DATE: 2001-07-24

; PRIOR APPLICATION NUMBER: US 60/243,046

; PRIOR FILING DATE: 2000-10-25

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 7

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-057-620-7

Query Match 86.7%; Score 26; DB 4; Length 8;

Best Local Similarity 83.3%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1;

QY 1 RKRRKR 6
|:|||||
Db 1 RKRRKR 6

RESULT 14

US-10-902-959-49

; Sequence 49, Application US/10902959

; Publication No. US20050059595A1

; GENERAL INFORMATION:

; APPLICANT: MCKERRACHER, LISA

; TITLE OF INVENTION: FUSION PROTEINS

; FILE REFERENCE: 06746-004-US-03

; CURRENT APPLICATION NUMBER: US/10/902,959

; CURRENT FILING DATE: 2004-08-02

; PRIOR APPLICATION NUMBER: CA 2,367,636

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: CA 2,362,004

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: CA 2,342,970

; PRIOR FILING DATE: 2001-04-12

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 49

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Amino acid sequence fused to C3 protein to created C3 Tat-short

US-10-902-959-49

Query Match 86.7%; Score 26; DB 5; Length 10;

Best Local Similarity 83.3%; Pred. No. 4.1e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1;

QY 1 RKRRKR 6
|:|||||
Db 3 RKRRR 8

```

; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,804
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-746-170-26

Query Match      86.7%; Score 26; DB 3; Length 13;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRKR 6
Db      2 RKQRK 7

RESULT 18
US-09-746-170-31
; Sequence 31, Application US/09746170
; Patent No. US20020127543A1
; GENERAL INFORMATION:
; APPLICANT: Walkers, Stephen
; APPLICANT: Karn, Jonathan
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,804
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-746-170-31

Query Match      86.7%; Score 26; DB 3; Length 13;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRKR 6
Db      2 RKQRK 7

RESULT 19
US-09-746-170-35
; Sequence 35, Application US/09746170
; Patent No. US20020127543A1
; GENERAL INFORMATION:
; APPLICANT: Walkers, Stephen
; APPLICANT: Karn, Jonathan
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,804
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-746-170-35

; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,804
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-746-170-26

Query Match      86.7%; Score 26; DB 5; Length 10;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRKR 6
Db      2 RKQRK 7

RESULT 16
US-10-983-169-11
; Sequence 11, Application US/10983169
; Publication No. US20050196383A1
; GENERAL INFORMATION:
; APPLICANT: Zurbriggen, Rinaldo E.
; TITLE OF INVENTION: Compositions and Methods for the Potentiation of Immune Responses
; FILE REFERENCE: 126442-100012
; CURRENT APPLICATION NUMBER: US/10/983,169
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,502
; PRIOR FILING DATE: 2003-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide derived from Apis mellifera
US-10-983-169-2

Query Match      86.7%; Score 26; DB 5; Length 10;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRKR 6
Db      2 RKQRK 7

RESULT 17
US-09-746-170-26
; Sequence 26, Application US/09746170
; Patent No. US20020127543A1
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Walkers, Stephen
US-09-746-170-26

Query Match      86.7%; Score 26; DB 5; Length 11;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRKR 6
Db      3 RKQRK 8

RESULT 17
US-09-746-170-26
; Sequence 26, Application US/09746170
; Patent No. US20020127543A1
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Walkers, Stephen
US-09-746-170-26
```



```
Query Match      86.7%; Score 26; DB 3; Length 13;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRKR 6
Db 2 RKRKQ 7

RESULT 20
US-09-746-170-37
; Sequence 37, Application US/09746170
; Patent No. US20020127543A1
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Walker, Stephen
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,804
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-746-170-37

Query Match      86.7%; Score 26; DB 3; Length 13;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRKR 6
Db 2 RKRQR 7

RESULT 21
US-10-983-169-3
; Sequence 3, Application US/10983169
; Publication No. US20050196383A1
; GENERAL INFORMATION:
; APPLICANT: Zurbriggen, Rinaldo E.
; TITLE OF INVENTION: Compositions and Methods for the Potentiation of Immune Responses
; FILE REFERENCE: 126442-100012
; CURRENT APPLICATION NUMBER: US/10/983,169
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US/09/517,502
; PRIOR FILING DATE: 2003-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide derived from Apis mellifera
US-10-983-169-3

Query Match      86.7%; Score 26; DB 5; Length 15;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRKR 6
Db 2 RKRQR 7

RESULT 22
```

```
US-10-983-169-10
; Sequence 10, Application US/10983169
; Publication No. US20050196383A1
; GENERAL INFORMATION:
; APPLICANT: Zurbriggen, Rinaldo E.
; TITLE OF INVENTION: Compositions and Methods for the Potentiation of Immune Responses
; FILE REFERENCE: 126442-100012
; CURRENT APPLICATION NUMBER: US/10/983,169
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US/09/517,502
; PRIOR FILING DATE: 2003-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Cys-Mel-Ova 257-64
US-10-983-169-10

Query Match      86.7%; Score 26; DB 5; Length 19;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRKR 6
Db 3 RKRQR 8

RESULT 23
US-09-809-790-7
; Sequence 7, Application US/09809790
; Patent No. US20020072102A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bairdur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,790
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
US-09-809-790-7

Query Match      83.3%; Score 25; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKRKR 6
Db 1 RKRKR 5

RESULT 24
US-09-809-790-8
; Sequence 8, Application US/09809790
; Patent No. US20020072102A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bairdur, Nand
; APPLICANT: Deisher, Theresa A.
```

; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,790
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
US-09-809-790-8

Query Match 83.3%; Score 25; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRRKR 6
Db 2 KRRKR 6

RESULT 25

US-09-809-617-7
; Sequence 7, Application US/09809617
; Patent No. US20020137178A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,617
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
US-09-809-617-7

Query Match 83.3%; Score 25; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRRKR 6
Db 1 KRRKR 5

RESULT 26

US-09-809-617-8
; Sequence 8, Application US/09809617
; Patent No. US20020137178A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/809,617
; CURRENT FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
US-09-809-617-8

Query Match 83.3%; Score 25; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRRKR 6
Db 2 KRRKR 6

RESULT 27

US-09-876-904A-360
; Sequence 360, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 360
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human PRDII-BF1 that binds to IFN-beta gene
; OTHER INFORMATION: promoter.
US-09-876-904A-360

Query Match 83.3%; Score 25; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRRRK 5
Db 2 KRRRK 6

RESULT 28

US-10-660-370-194
; Sequence 194, Application US/10660370
; Publication No. US20050064507A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, J. Stephen
; APPLICANT: National Institutes of Health
; TITLE OF INVENTION: Determining Kinase Specificity
; FILE REFERENCE: 1662.009US2
; CURRENT APPLICATION NUMBER: US/10/660,370
; CURRENT FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 640
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

Job time : 164 secs

; OTHER INFORMATION: A synthetic peptide
US-10-660-370-194

Query Match 83.3%; Score 25; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRK 6
DB 1 KRRK 5

RESULT 29
US-09-746-170-8
; Sequence 8, Application US/09746170
; Patent No. US20020127543A1
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Walker, Stephen
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR FILING DATE: 60/171,804
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-746-170-8

Query Match 83.3%; Score 25; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRRK 5
DB 6 KRRK 10

RESULT 30
US-09-746-170-17
; Sequence 17, Application US/09746170
; Patent No. US20020127543A1
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Walker, Stephen
; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
; FILE REFERENCE: 22620/1280
; CURRENT APPLICATION NUMBER: US/09/746,170
; CURRENT FILING DATE: 2000-12-22
; PRIOR FILING DATE: 60/171,804
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-746-170-17

Query Match 83.3%; Score 25; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRRK 5
DB 6 KRRK 10

Search completed: April 13, 2006, 08:53:22

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 13, 2006, 08:41:39 ; Search time 184 Seconds
(without alignments)
14.328 Million cell updates/sec

Title: US-09-816-688B-1
Perfect score: 30
Sequence: 1 RKRRKR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 897420

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	6	AAU09934	Aau09934 Synthetic
2	30	100.0	6	ADP09125	Adp09125 PACE-furi
3	30	100.0	8	ADK08902	Adk08902 Human pap
4	30	100.0	9	AAW42225	Aar42225 Anti-herp
5	30	100.0	9	AAW70502	Aar70502 Anti-cyto
6	30	100.0	9	AAW24810	Aaw24810 Anti-cyto
7	30	100.0	9	AAW25615	Aaw25615 Peptide #
8	30	100.0	9	ABR07953	AbR07953 Human can
9	30	100.0	9	ABR08153	AbR08153 Human can
10	30	100.0	9	ABR08722	AbR08722 Human can
11	30	100.0	9	ABR07954	AbR07954 Human can
12	30	100.0	9	ABR08474	AbR08474 Human can
13	30	100.0	9	ABR08536	AbR08536 Human can
14	30	100.0	9	ABR08558	AbR08558 Human can
15	30	100.0	9	ABR08701	AbR08701 Human can
16	30	100.0	9	ABR07558	AbR07558 Human can
17	30	100.0	9	ABR08154	AbR08154 Human can
18	30	100.0	9	ADK08966	Adk08966 Human pap
19	30	100.0	10	ABR08921	AbR08921 Human can
20	30	100.0	10	ABR08402	AbR08402 Human can
21	30	100.0	10	ABR08569	AbR08569 Human can
22	30	100.0	10	ABR08053	AbR08053 Human can
23	30	100.0	10	ABR08455	AbR08455 Human can
24	30	100.0	10	ABR08559	AbR08559 Human can

25	30	100.0	10	ABR07978	Human can
26	30	100.0	10	ABR08871	Human can
27	30	100.0	10	ABR08821	Human can
28	30	100.0	10	ABR08771	Human can
29	30	100.0	10	ABR08212	Human can
30	30	100.0	10	ABR07803	Human can
31	30	100.0	10	ABR07601	Human can
32	30	100.0	10	ABR08196	Human can
33	30	100.0	10	ABR08253	Human can
34	30	100.0	10	ADK09033	Human pap
35	30	100.0	10	ADK09030	Human pap
36	30	100.0	10	ADK09031	Human pap
37	30	100.0	10	ADK09032	Human pap
38	30	100.0	11	ABP54087	Abp54087 Transpore
39	30	100.0	11	ADC19832	Adc19832 Fluoresce
40	30	100.0	15	ABR32392	Human can
41	30	100.0	15	ABR32483	Human can
42	30	100.0	15	ABR32427	Human can
43	30	100.0	15	ABR32527	Human can
44	30	100.0	15	ABR32391	Human can
45	30	100.0	15	ABR32528	Human can
46	30	100.0	15	ADX58977	Rat tumou
47	30	100.0	18	ABR11544	Apollipop
48	30	100.0	21	AAW05023	Papilloma
49	27	90.0	6	AAW79064	Peptide w
50	27	90.0	6	ABR57040	Furin-rec
51	27	90.0	8	ABR74584	Transcrip
52	27	90.0	8	ADG27383	Lipin nuc
53	27	90.0	8	ADC22381	Nuclear l
54	27	90.0	8	ADF17317	Nuclear t
55	27	90.0	8	ADF86145	Human NLS
56	27	90.0	8	ADP43928	Nuclear l
57	27	90.0	8	AEA42036	GAG-bindi
58	27	90.0	9	AAW27778	Transacti
59	27	90.0	9	AAW42226	Anti-herp
60	27	90.0	9	AAW42224	Anti-herp
61	27	90.0	9	AAW42223	Anti-herp
62	27	90.0	9	AAW42217	Anti-herp
63	27	90.0	9	AAW70494	Anti-cyto
64	27	90.0	9	AAW70500	Anti-cyto
65	27	90.0	9	AAW70501	Anti-cyto
66	27	90.0	9	AAW70503	Anti-cyto
67	27	90.0	9	AAW24809	Anti-cyto
68	27	90.0	9	AAW24811	Anti-cyto
69	27	90.0	9	AAW24802	Anti-cyto
70	27	90.0	9	AAW24808	Anti-cyto
71	27	90.0	9	AAW25613	Peptide #
72	27	90.0	9	AAW25616	Peptide #
73	27	90.0	9	AAW25614	Peptide #
74	27	90.0	9	AAW25607	Peptide #
75	27	90.0	9	ABR28225	Human can
76	27	90.0	9	ABR28035	Human can
77	27	90.0	9	ABR27624	Human can
78	27	90.0	9	ABR27781	Human can
79	27	90.0	9	ABR28206	Human can
80	27	90.0	10	ABR27903	Human can
81	27	90.0	10	ABR28349	Human can
82	27	90.0	10	ABR27750	Human can
83	27	90.0	10	ABR28545	Human can
84	27	90.0	10	ABR27314	Human can
85	27	90.0	10	ABR27499	Human can
86	27	90.0	11	AAW28133	Cell-to-c
87	27	90.0	11	AAW28090	Cell-to-c
88	27	90.0	11	AAU78975	HNF-3 pep
89	27	90.0	12	AAW44186	Anti-herp
90	27	90.0	12	AAW44187	Anti-herp
91	27	90.0	12	AAU78946	HNF3 pept
92	27	90.0	13	AAW69773	RNA bindi
93	27	90.0	13	AAU06110	RNA bindi
94	27	90.0	14	AAW21506	Smooth mu
95	27	90.0	18	ABR11545	Apollipop
96	27	90.0	19	ABP82510	G protein
97	27	90.0	21	AAW20816	Human neu

98	27	90.0	21	4	ABB32457	Abb32457 Peptide #	KW	Bernard-Soulier's thrombasthenia; decreased clotting time.	
99	26	86.7	7	6	AAOI6743	AAOI6743 Nuclear 1	XX	Synthetic.	
100	26	86.7	8	5	ABG31280	ABG31280 Human fac	OS		
101	26	86.7	10	4	AAG86255	AAG86255 Saccharom	XX		
102	26	86.7	10	9	AD225756	AD225756 Peptide f	PN	WO200170763-A1.	
103	26	86.7	10	9	AEA47550	AEA47550 Peptide d	XX		
104	26	86.7	11	3	AB30411	AB30411 Nuclear 1	PD	27-SEP-2001.	
105	26	86.7	11	9	AEA47559	AEA47559 Peptide c	XX		
106	26	86.7	13	3	AY69769	AY69769 RNA bindi	PF	22-MAR-2001; 2001WO-US009355.	
107	26	86.7	13	3	AY69765	AY69765 RNA bindi	XX		
108	26	86.7	13	3	AY69771	AY69771 RNA bindi	PR	22-MAR-2000; 2000US-0191331P.	
109	26	86.7	13	3	AY69760	AY69760 RNA bindi	XX		
110	26	86.7	13	4	AAU06106	AAU06106 RNA bindi	PA	(CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.	
111	26	86.7	13	4	AAU06097	AAU06097 RNA bindi	XX		
112	26	86.7	13	4	AAU06108	AAU06108 RNA bindi	PI	High KA, Margaritis P, Camire RM;	
113	26	86.7	13	4	AAU06102	AAU06102 RNA bindi	XX	WPI; 2001-611468/70.	
114	26	86.7	13	8	ADU15719	ADU15719 MUC1-PD2	DR		
115	26	86.7	15	9	AEA47551	AEA47551 Peptide d	XX	Mutant blood clotting factors useful for treating a bleeding or clotting disorder in a subject, comprising a modified proteolytic cleavage site not normally present in the factor.	
116	26	86.7	18	9	ABE11553	ABE11553 Apolipop	PT	Claim 9; Page 41; 55pp; English.	
117	26	86.7	19	9	AEA47558	AEA47558 Amino aci	CC	The invention relates to a new composition comprising a recombinant polynucleotide that encodes a modified blood clotting factor (MBCF), where the modification comprises a proteolytic cleavage site not normally present in the factor, and where the factor is cleaved at the cleavage site when expressed in an animal cell. The new composition is useful for treating a bleeding or clotting disorder of a subject, preferably mammal especially human, having or at risk of having such a disorder, amenable to treatment with Factor VII, Factor VIII or Factor IX and caused by insufficient activity of expression of a vitamin-K dependent procoagulant, or by insufficient platelet aggregation. The disorder comprises haemophilia comprising haemophilia A or B, or Factor VII deficiency, Glanzmann's thrombasthenia or Bernard-Soulier's thrombasthenia. The subject produces inhibitory antibodies that bind to a clotting factor preferably Factor VIII or Factor IX. The composition of the invention is also useful for decreasing clotting time and for reducing the frequency or severity of bleeding in a subject. Unlike wild type Factor VII, MBCF comprises a Factor VII having increased activity, increased stability and decreased immunogenicity in vivo; and the secretion of the cleaved factor eliminates proteolytic cleavage during the blood clotting process. The present peptide sequence represents a synthetic proteolytic cleavage recognition site of the invention	
118	25	83.3	5	2	AAW26219	AAW26219 Fusion pr	CC		
119	25	83.3	5	6	AAE33758	AAE33758 Peptide u	XX		
120	25	83.3	6	3	AAV54459	AAV54459 Antigenic	PS		
121	25	83.3	6	3	AAV54458	AAV54458 Antigenic	XX		
122	25	83.3	6	4	AAU07191	AAU07191 Human dis	CC		
123	25	83.3	6	4	AAU07192	AAU07192 Human dis	CC		
124	25	83.3	6	5	ABB78131	ABB78131 Epitope b	CC		
125	25	83.3	6	5	ABB78132	ABB78132 Epitope b	CC		
126	25	83.3	6	9	AEA41490	AEA41490 Kappa B/V	CC		
127	25	83.3	6	9	AEA41455	AEA41455 GAG-bind	CC		
128	25	83.3	6	9	AEA42006	AEA42006 GAG-bind	CC		
129	25	83.3	6	9	AEA41454	AEA41454 GAG-bind	CC		
130	25	83.3	6	9	AEA41496	AEA41496 Kappa B/V	CC		
131	25	83.3	6	9	AEA42007	AEA42007 GAG-bind	CC		
132	25	83.3	7	2	AAV05442	AAV05442 Bronchodi	CC		
133	25	83.3	8	2	AAW02277	AAW02277 Small nuc	CC		
134	25	83.3	8	5	ABB74596	ABB74596 Transcrip	CC		
135	25	83.3	8	8	ADK08903	ADK08903 Human pap	CC		
136	25	83.3	8	9	AEA42005	AEA42005 GAG-bind	CC		
137	25	83.3	8	9	AEA41486	AEA41486 Kappa B/V	CC		
138	25	83.3	9	2	AAV05609	AAV05609 Peptide a	CC		
139	25	83.3	9	6	ABR07493	ABR07493 Human can	CC		
140	25	83.3	9	6	ABR07871	ABR07871 Human can	CC		
141	25	83.3	9	6	ABR08071	ABR08071 Human can	CC		
142	25	83.3	9	8	ADK08968	ADK08968 Human pap	CC		
143	25	83.3	9	8	ADK08967	ADK08967 Human pap	CC		
144	25	83.3	10	6	ABR08637	ABR08637 Human can	CC		
145	25	83.3	10	6	ABR07588	ABR07588 Human can	CC		
146	25	83.3	10	6	ABR08008	ABR08008 Human can	CC		
147	25	83.3	10	6	ABR08183	ABR08183 Human can	CC		
148	25	83.3	10	8	ADK09035	ADK09035 Human pap	CC		
149	25	83.3	10	8	ADK09034	ADK09034 Human pap	CC		
150	25	83.3	11	2	AAE28129	AAE28129 Cell-to-c	XX		
								Sequence 6 AA;	
								Query Match	
								Best Local Similarity	
								Matches	
								100.0%; Score 30; DB 4; Length 6;	
								6; Conservative	
								0; Mismatches	
								0; Indels	
								0; Gaps	
								0;	
QY	1	RKRRKR	6						
Db	1	RKRRKR	6						
								RESULT 2	
								ADF09125	
ID	ADF09125	standard; peptide; 6 AA.							
XX	AD								
AC	ADF09125;								
XX	AD								
DT	26-FEB-2004	(first entry)							
XX	AD								
DE	PACE-furin-like	protease cleavage site peptide SEQ ID NO:5.							
XX	human; factor VIII; FVIII;	variant; haemostatic; gene therapy;							
KW	haemophilia.								
KW	haemophilia.								
OS	Synthetic.								
XX	WO2003100053-A1.								
PN	WO2003100053-A1.								

ALIGNMENTS

RESULT 1		
AAU09934		
ID	AAU09934	standard; peptide; 6 AA.
XX	AAU09934;	
XX	18-JUN-2002	(first entry)
DT		
DE	Synthetic proteolytic cleavage recognition site peptide sequence #1.	
XX	Proteolytic cleavage recognition site; haemostatic; factor VII-agonist;	
KW	factor VIII-agonist; factor IX-agonist; modified blood clotting factor;	
KW	MBCF; bleeding disorder; clotting disorder; Factor VII; Factor VIII;	
KW	Factor IX; vitamin-K dependent procoagulant; platelet aggregation;	
KW	haemophilia; Glanzmann's thrombasthenia; antibody; immunogenicity;	

XX 04-DEC-2003.
 XX 22-MAY-2003; 2003WO-US016376.
 XX 22-MAY-2002; 2002US-0382486P.
 PR (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
 PA High KA, Camire RM;
 XX WPI; 2004-035147/03.
 DR New nucleic acid sequence encoding a biologically active recombinant
 PT human factor VIII variant, useful for preparing a composition for
 PT treating hemophilia.
 XX Claim 3; SEQ ID NO 5; 57pp; English.
 XX The present invention describes an isolated nucleic acid sequence
 CC encoding a biologically active recombinant human factor VIII (FVIII)
 CC variant comprising variants set forth in table 2 in the specification
 CC (see page 32-33). Also described: (1) a vector comprising the nucleic
 CC acid sequence; (2) an isolated modified human FVIII protein produced by
 CC expression of the nucleic acid; and (3) a method of treating haemophilia
 CC in a patient. Human FVIII has haemostatic activity, and can be used in
 CC gene therapy. The nucleic acid can be used for preparing a composition
 CC for treating haemophilia. The present sequence represents a PACB-furin-
 CC like protease cleavage site peptide, which is used in the exemplification
 CC of the present invention. The human FVIII gene is located on chromosome
 CC X, more specifically to Xq28.
 XX Sequence 6 AA;
 SQ Query Match 100.0%; Score 30; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. NO. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKRRKR 6
 DB 1 RKRRKR 6
 RESULT 3
 ADK08902
 ID ADK08902 standard; peptide; 8 AA.
 XX
 AC ADK08902;
 DT 06-MAY-2004 (first entry)
 XX Human papillomavirus peptide #957.
 DE pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection; HPV.
 XX Human papillomavirus.
 OS WO2004011650-A2.
 PN 05-FEB-2004.
 XX 24-JUL-2003; 2003WO-EP008112.
 PF 24-JUL-2002; 2002AT-00001124.
 PR 11-JUL-2003; 2003EP-00450171.
 XX (INTE-) INTERCELL AG.
 PA Mattner F, Schmidt W, Habel A;
 XX WPI; 2004-169243/16.
 DR
 XX

PT New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.
 XX Claim 18; Page 184; 220pp; English.
 XX This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
 CC invention.
 XX Sequence 8 AA;
 SQ Query Match 100.0%; Score 30; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. NO. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKRRKR 6
 DB 2 RKRRKR 7
 RESULT 4
 AAR42225
 ID AAR42225 standard; peptide; 9 AA.
 XX
 AC AAR42225;
 DT 25-MAR-2003 (revised)
 DT 17-MAY-1994 (first entry)
 XX
 DE Anti-herpetic peptide.
 XX Treatment; herpes virus infection; antiherpetic.
 KW Synthetic.
 OS WO9321941-A1.
 PN 11-NOV-1993.
 XX
 PD 21-APR-1993; 93WO-CA000166.
 PF 23-APR-1992; 92US-00872398.
 PR (KIRW/) KIRWOOD S D.
 PA (ALIX) ALLELIX BIOPHARMACEUTICALS INC.
 XX
 PI Twist M, Barnett RW, Summer-Smith M;
 XX WPI; 1993-368410/46.
 DR
 XX Compens. for treatment of herpes virus infections - contg.
 PT oligopeptide(s), esp. nona:D-arginine peptide, as active agent.
 PT Disclosure; Page 9; 36pp; English.
 XX The peptide may be used in a compen. for the treatment of herpes virus
 CC infection in humans or animals, this may be administered topically or
 CC systemically. The peptide is prepd. by conventional methods, e.g., by
 CC solid phase synthesis methods. (Updated on 25-MAR-2003 to correct PN
 CC field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 9 AA;
 SQ Query Match 100.0%; Score 30; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 2e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRKR 6
 Db 2 RRRKR 7

RESULT 5
 AAR70502
 ID AAR70502 standard; peptide; 9 AA.
 XX
 AC AAR70502;
 XX
 DT 04-JAN-1996 (first entry)
 XX
 DE Anti-cytomegalovirus peptide.
 XX
 KW Anti-cytomegalovirus; CMV; gancyclovir; foscarnet; AIDS; chemotherapy;
 KW tissue rejection therapy; treatment.
 XX
 OS Synthetic.
 XX
 PN W09511038-A1.
 XX
 PD 27-APR-1995.
 XX
 PF 21-OCT-1994; 94WO-CA000590.
 XX
 PR 22-OCT-1993; 93US-00139757.
 XX
 PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
 XX
 PI Twist M, Summer-Smith M;
 XX
 DR WPI; 1995-170038/22.
 XX
 DR WPI; 1995-170038/22.
 XX
 PT Use of peptide(s) for prepn. of anti-Cytomegalovirus compsn. - e.g.
 PT acetyl-[D-Arg]9-NH2.
 XX
 PS Disclosure; Page 9; 41pp; English.
 XX
 CC AAR70494-R70518 are anti-cytomegalovirus (CMV) peptides, they can be used
 CC to treat CMV infections, pref. in combination with other agents, e.g.
 CC gancyclovir and foscarnet. They are esp. effective in the treatment of
 CC immunocompromised patients, i.e. AIDS patients and patients undergoing
 CC chemo- and tissue rejection therapy
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRKR 6
 Db 2 RRRKR 7

RESULT 6
 AAW24810
 ID AAW24810 standard; peptide; 9 AA.
 XX
 AC AAW24810;
 XX
 DT 25-MAR-2003 (revised)
 DT 09-OCT-1997 (first entry)
 XX
 DE Anti-cytomegalovirus peptide #9.
 XX
 KW Cytomegalovirus; infection; immunocompromised patient; AIDS;
 KW acquired immunodeficiency syndrome.
 XX
 OS Synthetic.

XX FH Key Location/Qualifiers
 FT Misc-difference 1..9
 FT /note= "D-form residues; the N-terminal residue is
 FT preferably acylated and the C-terminal residue is
 FT preferably amidated"
 XX
 PN US5633230-A.
 XX
 PD 27-MAY-1997.
 XX
 PF 31-OCT-1994; 94US-00332518.
 XX
 PR 24-OCT-1990; 90US-00602953.
 PR 23-OCT-1991; 91US-00779735.
 PR 23-APR-1992; 92US-00872398.
 PR 22-DEC-1992; 92US-00995742.
 PR 22-OCT-1993; 93US-00139757.
 XX
 PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
 XX
 PI Twist M, Summer-Smith M;
 XX
 DR WPI; 1997-309327/28.
 XX
 PT New cationic peptide rich in D-arginine residues - useful for treating
 PT cytomegalovirus infections, e.g. in immuno-compromised AIDS patients.
 XX
 PS Disclosure; Col 19; 20pp; English.
 XX
 CC Peptides AAW24802-26 are examples of peptides of formula: R1-X-R2, where
 CC R1 = H or a N-terminal protecting group, especially an acyl group; R2 =
 CC OH or a C-terminal protecting group, especially an amide group; and X is
 CC an oligopeptide chain of 'n' D-amino acid residues. The oligopeptide
 CC preferably has a net positive charge of n, n-1 or n-2. It comprises D-Arg
 CC residues with a maximum of 3 other D-residue. The peptides are used for
 CC treating cytomegalovirus infections in immunocompromised patients,
 CC especially AIDS patients. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRKR 6
 Db 2 RRRKR 7

RESULT 7
 AAW25615
 ID AAW25615 standard; peptide; 9 AA.
 XX
 AC AAW25615;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-NOV-1997 (first entry)
 XX
 DE Peptide #10, inhibits HIV replication.
 XX
 KW Inhibition; HIV; human immunodeficiency virus; replication.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..9
 FT /note= "Opt. D-form residues"
 XX
 PN US5646120-A.
 XX
 PD 08-JUL-1997.
 XX

PF 14-DEC-1994; 94US-00357056.
XX
PR 24-OCT-1990; 90US-00602953.
PR 23-OCT-1991; 91US-00779735.
XX
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
XX
PI Sonnenberg N, Reid LS, Barnett RW, Sumner-Smith M;
XX
DR WPI; 1997-362969/33.
XX
XX New D-arginine oligomers - useful as antiviral agents, especially against
PT HIV.
PT
PS Disclosure; Col 6; 14pp; English.
XX
XX The sequences given in AAW25606-33 represent peptides which can be used
CC in D-Arginine oligomers of formula: R1-X-R2 (I). R1 = H, lower alkanoyl,
CC a deaminated amino acid or a N-terminal protecting group; R2 = OH, lower
CC alkyl, amino, mono- or di(lower alkyl)amino, a decarboxylated amino acid
CC or a C-terminal protecting group; X = a chain of 7-12 D-arginine
CC residues. The compounds are useful as antiviral agents, especially for
CC inhibiting HIV replication. They are administered in intravenous doses of
CC 1 microg/kg to 10 mg/kg, especially 0.1-5 mg/kg. (Updated on 25-MAR-2003
CC to correct PF field.)
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 30; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRRR 6
DB 2 RRRRR 7
RESULT 8
ABR07953
ID ABR07953 standard; peptide; 9 AA.
AC ABR07953;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 151PIC7A HLA peptide #488.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.

XX
PS Claim 13; Page 191; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 30; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRRR 6
DB 4 RRRRR 9
RESULT 9
ABR08153
ID ABR08153 standard; peptide; 9 AA.
XX
AC ABR08153;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 151PIC7A HLA peptide #688.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 193; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or

CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRKR 6
Db 4 RRRKR 9

RESULT 10
ABR08722
ID ABR08722 standard; peptide; 9 AA.
AC ABR08722;
DT 19-MAY-2003 (first entry)
DE Human cancer-related protein 151P1C7A HLA peptide #1257.
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX Homo sapiens.
OS WO200283921-A2.
PN 24-OCT-2002.
PD 10-APR-2002; 2002WO-US011654.
PF 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
PI WPI; 2003-075555/07.
DR New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response in
XX cancer patients.
XX Claim 13; Page 199; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention
XX Sequence 9 AA;

Query Match 100.0%; Score 30; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRRKR 6
Db 3 RRRKR 8

RESULT 11
ABR07954
ID ABR07954 standard; peptide; 9 AA.
XX ABR07954;
AC ABR07954;
DT 19-MAY-2003 (first entry)
DE Human cancer-related protein 151P1C7A HLA peptide #489.
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX Homo sapiens.
OS WO200283921-A2.
PN 24-OCT-2002.
PD 10-APR-2002; 2002WO-US011654.
PF 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
PI WPI; 2003-075555/07.
DR New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response in
XX cancer patients.
XX Claim 13; Page 191; 1021pp; English.
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention
XX Sequence 9 AA;

Query Match 100.0%; Score 30; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRKR 6
Db 1 RRRKR 6

RESULT 12
ABR08474
ID ABR08474 standard; peptide; 9 AA.

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XX ABR08474;
AC
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 151P1C7A HLA peptide #1009.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Farris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 197; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db |||||
3 RKRRKR 8

RESULT 13
ABR08536
ID ABR08536 standard; peptide; 9 AA.
XX
AC ABR08536;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 151P1C7A HLA peptide #1071.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX

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OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Farris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 197; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db |||||
2 RKRRKR 7

RESULT 14
ABR08558
ID ABR08558 standard; peptide; 9 AA.
XX
AC ABR08558;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 151P1C7A HLA peptide #1093.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
XX

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PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 197; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 30; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RKRRKR 6
Db |||||
4 RKRRKR 9
RESULT 15
ABR08701
ID ABR08701 standard; peptide; 9 AA.
XX
AC ABR08701;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 151P1C7A HLA peptide #1236.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of

PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 199; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 30; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RKRRKR 6
Db |||||
2 RKRRKR 7
RESULT 16
ABR07558
ID ABR07558 standard; peptide; 9 AA.
XX
AC ABR07558;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 151P1C7A HLA peptide #93.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 187; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 DB 4 RKRRKR 9

RESULT 17
 ABR08154
 ID ABR08154 standard; peptide; 9 AA.

AC ABR08154;
 DT 19-MAY-2003 (first entry)
 XX Human cancer-related protein 151P1C7A HLA peptide #689.
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX Homo sapiens.
 OS WO200283921-A2.
 PN 24-OCT-2002.
 PD 10-APR-2002; 2002WO-US011654.
 PF 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX (AGEN-) AGENSYS INC.
 PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 PI WPI; 2003-075555/07.

DR New composition comprising a substance that modulates the structure of
 XX proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX Claim 13; Page 193; 1021pp; English.

CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 DB 1 RKRRKR 6

RESULT 18
 ADK08966
 ID ADK08966 standard; peptide; 9 AA.
 AC ADK08966;
 DT 06-MAY-2004 (first entry)
 XX Human papillomavirus peptide #1021.
 DE pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection; HPV.
 XX Human papillomavirus.
 OS WO2004011650-A2.
 PN 05-FEB-2004.
 PD 24-JUL-2003; 2003WO-EP008112.
 PF 24-JUL-2002; 2002AT-00001124.
 PR 11-JUL-2003; 2003EP-00450171.
 XX (INTE-) INTERCELL AG.
 PA Mattner F, Schmidt W, Habel A;
 PI WPI; 2004-169243/16.

DR New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.
 XX Claim 18; Page 184; 220pp; English.

CC This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
 CC invention.
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 30; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 DB 3 RKRRKR 8

RESULT 19
 ABR08921
 ID ABR08921 standard; peptide; 10 AA.
 XX ABR08921;
 AC

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XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 151PIC7A HLA peptide #1456.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX CC New composition comprising a substance that modulates the structure of
XX CC proteins and polynucleotides, useful for therapeutic, prognostic and
XX CC diagnostic reagents for eliciting cellular or humoral immune response in
XX CC cancer patients.
XX PS Claim 13; Page 201; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 10 AA;
XX CC Query Match 100.0%; Score 30; DB 6; Length 10;
XX CC Best Local Similarity 100.0%; Pred. No. 86;
XX CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRKR 6
DB 4 RRRKR 9
RESULT 20
ABR08402
ID ABR08402 standard; peptide; 10 AA.
XX AC ABR08402;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 151PIC7A HLA peptide #937.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX CC New composition comprising a substance that modulates the structure of
XX CC proteins and polynucleotides, useful for therapeutic, prognostic and
XX CC diagnostic reagents for eliciting cellular or humoral immune response in
XX CC cancer patients.
XX PS Claim 13; Page 201; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 10 AA;
XX CC Query Match 100.0%; Score 30; DB 6; Length 10;
XX CC Best Local Similarity 100.0%; Pred. No. 86;
XX CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRKR 6
DB 4 RRRKR 9
RESULT 20
ABR08402
ID ABR08402 standard; peptide; 10 AA.
XX AC ABR08402;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 151PIC7A HLA peptide #937.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX CC New composition comprising a substance that modulates the structure of
XX CC proteins and polynucleotides, useful for therapeutic, prognostic and
XX CC diagnostic reagents for eliciting cellular or humoral immune response in
XX CC cancer patients.
XX PS Claim 13; Page 201; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 10 AA;
XX CC Query Match 100.0%; Score 30; DB 6; Length 10;
XX CC Best Local Similarity 100.0%; Pred. No. 86;
XX CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRKR 6
DB 3 RRRKR 8
RESULT 21
ABR08569
ID ABR08569 standard; peptide; 10 AA.
XX AC ABR08569;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 151PIC7A HLA peptide #1104.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX CC New composition comprising a substance that modulates the structure of
XX CC proteins and polynucleotides, useful for therapeutic, prognostic and
XX CC diagnostic reagents for eliciting cellular or humoral immune response in
XX CC cancer patients.
XX PS Claim 13; Page 196; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 10 AA;
XX CC Query Match 100.0%; Score 30; DB 6; Length 10;
XX CC Best Local Similarity 100.0%; Pred. No. 86;
XX CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRKR 6
DB 3 RRRKR 8
```

PA (AGEN-) AGENSYS INC.
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 DR WPI; 2003-075555/07.
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX Claim 13; Page 198; 1021pp; English.
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX Sequence 10 AA;
 SQ Query Match 100.0%; Score 30; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 DB 3 RKRRKR 8

RESULT 22
 ABR08053
 ID ABR08053 standard; peptide; 10 AA.
 AC ABR08053;
 DT 19-MAY-2003 (first entry)
 XX Human cancer-related protein 151P1C7A HLA peptide #588.
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX Homo sapiens.
 OS WO200283921-A2.
 PN 24-OCT-2002.
 XX 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX (AGEN-) AGENSYS INC.
 PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX WPI; 2003-075555/07.
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in

PT cancer patients.
 XX Claim 13; Page 192; 1021pp; English.
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX Sequence 10 AA;
 SQ Query Match 100.0%; Score 30; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 DB 2 RKRRKR 7

RESULT 23
 ABR08455
 ID ABR08455 standard; peptide; 10 AA.
 AC ABR08455;
 DT 19-MAY-2003 (first entry)
 XX Human cancer-related protein 151P1C7A HLA peptide #990.
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX Homo sapiens.
 OS WO200283921-A2.
 PN 24-OCT-2002.
 XX 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX (AGEN-) AGENSYS INC.
 PA Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX WPI; 2003-075555/07.
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX Claim 13; Page 196; 1021pp; English.
 XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 30; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRKR 6
Db 4 RRRKR 9

RESULT 24
ABR08599
ID ABR08599 standard; peptide; 10 AA.

XX ABR08599;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 151P1C7A HLA peptide #1134.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.

XX 10-APR-2001; 2001US-0283112P.

XX 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of

XX proteins and polynucleotides, useful for therapeutic, prognostic and

XX diagnostic reagents for eliciting cellular or humoral immune response in

XX cancer patients.

XX Claim 13; Page 198; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and

XX proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and

XX proteins are useful for eliciting a humoral or cellular immune response.

XX The genes are useful as probes and primers for the amplification and/or

XX detection of genes, mRNAs or their fragments, as reagents for the

XX diagnosis and/or prognosis of cancer, as coding sequences capable of

XX directing the expression of the protein, as tools for modulating or

XX inhibiting the expression of genes and/or translation of transcripts, and

Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRKR 6
Db 4 RRRKR 9

RESULT 25
ABR07978
ID ABR07978 standard; peptide; 10 AA.

XX ABR07978;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 151P1C7A HLA peptide #513.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.

XX 10-APR-2001; 2001US-0283112P.

XX 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of

XX proteins and polynucleotides, useful for therapeutic, prognostic and

XX diagnostic reagents for eliciting cellular or humoral immune response in

XX cancer patients.

XX Claim 13; Page 192; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and

XX proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and

XX proteins are useful for eliciting a humoral or cellular immune response.

XX The genes are useful as probes and primers for the amplification and/or

XX detection of genes, mRNAs or their fragments, as reagents for the

XX diagnosis and/or prognosis of cancer, as coding sequences capable of

XX directing the expression of the protein, as tools for modulating or

XX inhibiting the expression of genes and/or translation of transcripts, and

XX as therapeutic agents. The proteins and peptides are useful as

XX therapeutic, prognostic and diagnostic reagents for cancer. The present

XX sequence is a human leukocyte antigen (HLA) peptide, used in an example

XX from the invention

XX Sequence 10 AA;

Query Match 100.0%; Score 30; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRKR 6
Db 5 RRRKR 10

RESULT 26
ABR08871


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ID ABR08871 standard; peptide; 10 AA.
XX
AC ABR08871;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 151P1C7A HLA peptide #1406.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 201; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 30; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db |||||
4 RKRRKR 9

RESULT 27
ABR08821
ID ABR08821 standard; peptide; 10 AA.
XX
AC ABR08821;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 151P1C7A HLA peptide #1356.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX

ID ABR08871 standard; peptide; 10 AA.
XX
AC ABR08871;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 151P1C7A HLA peptide #1306.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 200; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 30; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db |||||
4 RKRRKR 9

RESULT 28
ABR08771
ID ABR08771 standard; peptide; 10 AA.
XX
AC ABR08771;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 151P1C7A HLA peptide #1306.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.

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PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response in
XX PT cancer patients.
XX PS Claim 13; Page 200; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 10 AA;

Query Match 100.0%; Score 30; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRKRK 6
Db 3 RKRKRK 8

RESULT 29
ABR08212
ID ABR08212 standard; peptide; 10 AA.
XX AC ABR08212;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 151P1C7A HLA peptide #747.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response in
XX PT cancer patients.
XX PS Claim 13; Page 190; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 10 AA;

Query Match 100.0%; Score 30; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRKRK 6
Db 3 RKRKRK 8

RESULT 30
ABR07803
ID ABR07803 standard; peptide; 10 AA.
XX AC ABR07803;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 151P1C7A HLA peptide #338.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response in
XX PT cancer patients.
XX PS Claim 13; Page 190; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 10 AA;

Query Match 100.0%; Score 30; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRKRK 6
Db 2 RKRKRK 7

```

CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 30; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKRRKR 6
 |||||
 Db 4 RKRRKR 9

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 Job time : 190 secs

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OM protein - protein search, using sw model

Run on: April 13, 2006, 08:49:20 ; Search time 46 Seconds
(without alignments)
10.784 Million cell updates/sec

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Perfect score: 30
Sequence: 1 KRKRK 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 229350

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RB COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	6	1 US-08-487-037-5	Sequence 5, Appli
2	30	100.0	9	1 US-08-332-518-10	Sequence 10, Appl
3	30	100.0	9	1 US-08-378-709-11	Sequence 11, Appl
4	30	100.0	21	1 US-07-678-974D-66	Sequence 66, Appl
5	30	100.0	21	1 US-08-945-168-72	Sequence 72, Appl
6	27	90.0	8	2 US-10-028-056-25	Sequence 25, Appl
7	27	90.0	9	1 US-08-332-518-2	Sequence 2, Appli
8	27	90.0	9	1 US-08-332-518-8	Sequence 8, Appli
9	27	90.0	9	1 US-08-332-518-9	Sequence 9, Appli
10	27	90.0	9	1 US-08-332-518-11	Sequence 11, Appl
11	27	90.0	9	1 US-08-378-709-3	Sequence 3, Appli
12	27	90.0	9	1 US-08-378-709-9	Sequence 9, Appli
13	27	90.0	9	1 US-08-378-709-10	Sequence 10, Appl
14	27	90.0	9	1 US-08-378-709-12	Sequence 12, Appl
15	27	90.0	11	4 PCT-US91-08328-15	Sequence 15, Appl
16	27	90.0	11	4 PCT-US91-08328-21	Sequence 21, Appl
17	27	90.0	12	1 US-08-378-709-31	Sequence 31, Appl
18	27	90.0	13	2 US-09-325-601-50	Sequence 50, Appl
19	26	86.7	13	2 US-09-325-601-37	Sequence 37, Appl
20	26	86.7	13	2 US-09-325-601-42	Sequence 42, Appl
21	26	86.7	13	2 US-09-325-601-46	Sequence 46, Appl
22	26	86.7	13	2 US-09-325-601-48	Sequence 48, Appl
23	25	83.3	5	1 US-08-595-043A-30	Sequence 30, Appl
24	25	83.3	6	2 US-09-351-414-7	Sequence 7, Appli
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86	24	80.0	8	2 US-10-209-421-25	Sequence 25, Appl
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102 24 80.0 9 1 US-08-357-056-5
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148 24 80.0 10 2 US-09-949-474A-13
149 24 80.0 10 4 PCT-US91-08328-30
150 24 80.0 11 1 US-08-332-518-25
151 24 80.0 11 1 US-08-482-880-13

ALIGNMENTS

RESULT 1
US-08-487-037-5
; Sequence 5, Application US/08487037
; Patent No. 5795863
; GENERAL INFORMATION:
; APPLICANT: Wolf, David L.
; TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; Sequence 23, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 10, Appl
Sequence 11, Appl
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Sequence 19, Appl
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Sequence 29, Appl
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Sequence 13, Appl
Sequence 30, Appl
Sequence 25, Appl
Sequence 13, Appl
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,037
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Adlet, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 2803-0002.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-487-037-5
Query Match 100.0% Score 30; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRRR 6
Db 1 RRRRR 6
RESULT 2
US-08-332-518-10
; Sequence 10, Application US/08332518
; Patent No. 5633230
; GENERAL INFORMATION:
; APPLICANT: TWIST, Michael
; TITLE OF INVENTION: TREATMENT OF CYTOMEGALOVIRUS INFECTION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,518
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,757
; FILING DATE: 22-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,398
; FILING DATE: 23-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/602,953
; FILING DATE: 24-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,742
; FILING DATE: 22-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,318

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; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/266/ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-332-518-10

Query Match 100.0%; Score 30; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 2 RKRRKR 7

RESULT 3
US-08-378-709-11
; Sequence 11, Application US/08378709
; Patent No. 5831001
; GENERAL INFORMATION:
; APPLICANT: TWIST, Michael
; APPLICANT: BARNETT, Richard
; APPLICANT: REID, Lorne
; APPLICANT: SUMNER-SMITH, Martin
; TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,709
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,398
; FILING DATE: 23-APR-1992
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/602,953
; FILING DATE: 24-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/176 ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid

; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/266/ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-332-518-10

Query Match 100.0%; Score 30; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 2 RKRRKR 7

RESULT 4
US-07-678-974D-66
; Sequence 66, Application US/07678974D
; Patent No. 5629146
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERMAN & AISENBERG
; STREET: 1730 RHODE ISLAND AVENUE, N.W.,
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-3186
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/678,974D
; FILING DATE: 25-JUN-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: AISENBERG, Irwin M.
; REGISTRATION NUMBER: 19,007
; REFERENCE/DOCKET NUMBER: SG19171
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-293-1404
; TELEFAX: 202-872-0493
; TELEX: 440 069 AIS UI
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-07-678-974D-66

Query Match 100.0%; Score 30; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 4 RKRRKR 9

RESULT 5
US-08-945-168-72
; Sequence 72, Application US/08945168
; Patent No. 5989548
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; TITLE OF INVENTION: PEPTIDE-BASED VACCINE AGAINST PAPILLOMA
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
```

ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,168
FILING DATE: 18-DEC-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE96/00533
FILING DATE: 23-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9501512-9
FILING DATE: 24-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7752-0002-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-945-168-72

Query Match 100.0%; Score 30; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRKR 6
Db 4 RRRKR 9

RESULT 6
US-10-028-056-25
Sequence 25, Application US/10028056
Patent No. 6869766
GENERAL INFORMATION:
APPLICANT: REUE, KAREN
TITLE OF INVENTION: A NOVEL GENE ASSOCIATED WITH REGULATION OF ADIPOSY AND INSULIN
FILE REFERENCE: 407T-898010US
CURRENT APPLICATION NUMBER: US/10/028,056
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,772
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 25
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-028-056-25

Query Match 90.0%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRKR 6
Db 4 RRRKR 9

Db 1 KRRKR 6
RESULT 7
US-08-332-518-2
Sequence 2, Application US/08332518
Patent No. 5633230
GENERAL INFORMATION:
APPLICANT: TWIST, Michael
TITLE OF INVENTION: SUMMER-SMITH, Martin
SOFTWARE: PatentIn Release #1.0, Version #1.30
NUMBER OF SEQUENCES: 26
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,518
FILING DATE: 31-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,757
FILING DATE: 22-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,398
FILING DATE: 23-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,735
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/602,953
FILING DATE: 24-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,742
FILING DATE: 22-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,318
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/266/ALLE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-332-518-2

Query Match 90.0%; Score 27; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRKR 6
Db 2 KRRKR 7

RESULT 8
US-08-332-518-8

; Sequence 8, Application US/08332518
; Patent No. 5633230
; GENERAL INFORMATION:
; APPLICANT: TWIST, Michael
; APPLICANT: SUMNER-SMITH, Martin
; TITLE OF INVENTION: TREATMENT OF CYTOMEGALOVIRUS INFECTION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,518
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,757
; FILING DATE: 22-OCT-1993
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,398
; FILING DATE: 23-APR-1992
; APPLICATION NUMBER: US 07/602,953
; FILING DATE: 24-OCT-1990
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,742
; FILING DATE: 22-DEC-1992
; APPLICATION NUMBER: US 07/872,318
; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/266/ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-332-518-8

Query Match 90.0%; Score 27; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RKRKR 6
Db 1 RKRKR 6

RESULT 9
US-08-332-518-9
; Sequence 9, Application US/08332518
; Patent No. 5633230
; GENERAL INFORMATION:
; APPLICANT: TWIST, Michael
; APPLICANT: SUMNER-SMITH, Martin

; TITLE OF INVENTION: TREATMENT OF CYTOMEGALOVIRUS INFECTION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,518
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,757
; FILING DATE: 22-OCT-1993
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,398
; FILING DATE: 23-APR-1992
; APPLICATION NUMBER: US 07/602,953
; FILING DATE: 24-OCT-1990
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,742
; FILING DATE: 22-DEC-1992
; APPLICATION NUMBER: US 07/872,318
; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/266/ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-332-518-9

Query Match 90.0%; Score 27; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RKRKR 6
Db 2 RKRKR 7

RESULT 10
US-08-332-518-11
; Sequence 11, Application US/08332518
; Patent No. 5633230
; GENERAL INFORMATION:
; APPLICANT: TWIST, Michael
; APPLICANT: SUMNER-SMITH, Martin
; TITLE OF INVENTION: TREATMENT OF CYTOMEGALOVIRUS INFECTION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500

```

; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,518
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,757
; FILING DATE: 22-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,398
; FILING DATE: 23-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/602,953
; FILING DATE: 24-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,742
; FILING DATE: 22-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,318
; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/266/ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-332-518-11

Query Match          90.0%; Score 27; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. NO. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KRRKR 6
Db       2 RRRKR 7

RESULT 11
US-08-378-709-3
; Sequence 3, Application US/08378709
; Patent No. 5831001
; GENERAL INFORMATION:
; APPLICANT: TWIST, Michael
; APPLICANT: BARNETT, Richard
; APPLICANT: REID, Lorne
; APPLICANT: SUMNER-SMITH, Martin
; TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA

```

```

; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,709
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,398
; FILING DATE: 23-APR-1992
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/602,953
; FILING DATE: 24-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/176 ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 895149
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-378-709-3

Query Match          90.0%; Score 27; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. NO. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KRRKR 6
Db       2 KRRKR 7

RESULT 12
US-08-378-709-9
; Sequence 9, Application US/08378709
; Patent No. 5831001
; GENERAL INFORMATION:
; APPLICANT: TWIST, Michael
; APPLICANT: BARNETT, Richard
; APPLICANT: REID, Lorne
; APPLICANT: SUMNER-SMITH, Martin
; TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,709
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,398
; FILING DATE: 23-APR-1992
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/602,953
; FILING DATE: 24-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/176 ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 895149
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-378-709-3

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/ FILING DATE: 23-OCT-1991
/ PRIOR APPLICATION DATA: US 07/602,953
/ APPLICATION NUMBER: US 07/602,953
/ FILING DATE: 24-OCT-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 16777/176 ALLE
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)836-9300
/ TELEFAX: (703)683-4109
/ TELEX: 899149
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-378-709-9

Query Match          90.0%; Score 27; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RKRRKR 6
DB      1 RKRRR 6

RESULT 13
US-08-378-709-10
; Sequence 10, Application US/08378709
; Patent No. 5831001
; GENERAL INFORMATION:
; APPLICANT: TWIST, Michael
; APPLICANT: BARNETT, Richard
; APPLICANT: REID, Lorne
; APPLICANT: SUMNER-SMITH, Martin
; TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,709
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,398
; FILING DATE: 23-APR-1992
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/602,953
; FILING DATE: 24-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/176 ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-378-709-9

Query Match          90.0%; Score 27; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RKRRKR 6
DB      1 RKRRR 6
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/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-378-709-10

Query Match          90.0%; Score 27; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RKRRKR 6
DB      2 RKRRR 7

RESULT 14
US-08-378-709-12
; Sequence 12, Application US/08378709
; Patent No. 5831001
; GENERAL INFORMATION:
; APPLICANT: TWIST, Michael
; APPLICANT: BARNETT, Richard
; APPLICANT: REID, Lorne
; APPLICANT: SUMNER-SMITH, Martin
; TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,709
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,398
; FILING DATE: 23-APR-1992
; APPLICATION NUMBER: US 07/779,735
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/602,953
; FILING DATE: 24-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/176 ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-378-709-12

Query Match          90.0%; Score 27; DB 1; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RKRRKR 6
DB      2 RKRRR 7
```

RESULT 15
PCT-US91-08328-15
; Sequence 15, Application PC/TUS9108328
; GENERAL INFORMATION:
; APPLICANT: Ruggeri, Zaverio M.
; TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; STREET: Eugene Moroz, MORGAN & FINNEGAN
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: PCT/US91/08328
; FILING DATE: 19911107
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/610,363
; FILING DATE: 07-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Moroz, Eugene
; REGISTRATION NUMBER: 25,237
; REFERENCE/DOCKET NUMBER: 1198 4079PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Cross-links
; LOCATION: 5..>11
; OTHER INFORMATION: /note= "Sequence linked by
; OTHER INFORMATION: interchain amide bond at Lys residue with Glu
; OTHER INFORMATION: residue on Arg4-Glu-Arg-Ser-Arg-Gly-Asp-Val
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 28-JUL-1987
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US B1 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 03-JUL-1990
PCT-US91-08328-15
Query Match 90.0%; Score 27; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRR 6
|:|:|:|
DB 1 RRRRR 6

RESULT 16
PCT-US91-08328-21
; Sequence 21, Application PC/TUS9108328
; GENERAL INFORMATION:

; APPLICANT: Ruggeri, Zaverio M.
; APPLICANT: Houghten, Richard A.
; TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: PCT/US91/08328
; FILING DATE: 19911107
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/610,363
; FILING DATE: 07-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Moroz, Eugene
; REGISTRATION NUMBER: 25,237
; REFERENCE/DOCKET NUMBER: 1198 4079PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Cross-links
; LOCATION: 2..>11
; OTHER INFORMATION: /note= "Sequence linked by
; OTHER INFORMATION: interchain amide bond at Lys residue with Glu
; OTHER INFORMATION: residue on Arg-Glu-Arg4-Ser-Arg-Gly-Asp-Val"
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 28-JUL-1987
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US B1 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 03-JUL-1990
PCT-US91-08328-21
Query Match 90.0%; Score 27; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRR 6
|:|:|:|
DB 1 RRRRR 6

RESULT 17
US-08-378-709-31
; Sequence 31, Application US/08378709
; Patent No. 5831001
; GENERAL INFORMATION:
; APPLICANT: TWIST, Michael
; APPLICANT: BARNETT, Richard
; APPLICANT: REID, Lorne

APPLICANT: SUMNER-SMITH, Martin
TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,709
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,398
FILING DATE: 23-APR-1992
APPLICATION NUMBER: US 07/779,735
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/602,953
FILING DATE: 24-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/176 ALLE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
SEQUENCE FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-378-709-31

Query Match 90.0%; Score 27; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 96;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
DB 4 KRRKR 9

RESULT 18

US-09-325-601-50
Sequence 50, Application US/09325601
Patent No. 6573045
GENERAL INFORMATION:
APPLICANT: Karn
APPLICANT: Prescott

TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
FILE REFERENCE: 3950/81235
CURRENT APPLICATION NUMBER: US/09/325,601
CURRENT FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
OTHER INFORMATION: Q, R-pentapeptide library
US-09-325-601-50

Query Match 90.0%; Score 27; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 96;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match 90.0%; Score 27; DB 2; Length 13;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
DB 2 RRRRR 7

RESULT 19

US-09-325-601-37
Sequence 37, Application US/09325601
Patent No. 6573045
GENERAL INFORMATION:
APPLICANT: Karn
APPLICANT: Prescott
TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
FILE REFERENCE: 3950/81235
CURRENT APPLICATION NUMBER: US/09/325,601
CURRENT FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 37
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
OTHER INFORMATION: Q, R-pentapeptide library
US-09-325-601-37

Query Match 86.7%; Score 26; DB 2; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
DB 2 RKQKR 7

RESULT 20

US-09-325-601-42
Sequence 42, Application US/09325601
Patent No. 6573045
GENERAL INFORMATION:
APPLICANT: Karn
APPLICANT: Prescott

TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
FILE REFERENCE: 3950/81235
CURRENT APPLICATION NUMBER: US/09/325,601
CURRENT FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
OTHER INFORMATION: Q, R-pentapeptide library
US-09-325-601-42

Query Match 86.7%; Score 26; DB 2; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
DB 2 RKQKR 7

RESULT 21

US-09-325-601-46

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; Sequence 46, Application US/09325601
; Patent No. 6573045
; GENERAL INFORMATION:
; APPLICANT: Karn
; APPLICANT: Prescott
; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
; FILE REFERENCE: 3950/81235
; CURRENT APPLICATION NUMBER: US/09/325,601
; CURRENT FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
; OTHER INFORMATION: Q, R-pentapeptide library
US-09-325-601-46

Query Match      86.7%; Score 26; DB 2; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRRKR 6
Db 2 KRRKQ 7

RESULT 22
US-09-325-601-48
; Sequence 48, Application US/09325601
; Patent No. 6573045
; GENERAL INFORMATION:
; APPLICANT: Karn
; APPLICANT: Prescott
; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
; FILE REFERENCE: 3950/81235
; CURRENT APPLICATION NUMBER: US/09/325,601
; CURRENT FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
; OTHER INFORMATION: Q, R-pentapeptide library
US-09-325-601-48

Query Match      86.7%; Score 26; DB 2; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRRKR 6
Db 2 KRRKQ 7

RESULT 23
US-08-595-043A-30
; Sequence 30, Application US/08595043A
; Patent No. 5935824
; GENERAL INFORMATION:
; APPLICANT: SCARLATO, GREGORY D.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESS: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
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; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,043A
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: SGAR-00371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-595-043A-30

Query Match      83.3%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KRRK 5
Db 1 KRRK 5

RESULT 24
US-09-351-414-7
; Sequence 7, Application US/09351414
; Patent No. 6265199
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baindur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/351,414
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
US-09-351-414-7

Query Match      83.3%; Score 25; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRRKR 6
Db 1 KRRKR 5

RESULT 25
US-09-351-414-8
; Sequence 8, Application US/09351414
; Patent No. 6265199
; GENERAL INFORMATION:
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; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baindur, Nand
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/09/351,414
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
US-09-351-414-8

Query Match      83.3%; Score 25; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KRRKR 6
DB      2 KRRKR 6

RESULT 26
US-08-249-387-6
; Sequence 6, Application US/08249387
; Patent No. 5681700
; GENERAL INFORMATION:
; APPLICANT: Reichlin, Morris
; APPLICANT: Koren, Eugen
; TITLE OF INVENTION: Assay for Pathogenicity of Anti-DNA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,387
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRP145
; TELEPHONE: (404) 815-6508
; TELEFAX: (404) 815-6555
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-249-387-6

Query Match      83.3%; Score 25; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KRRKR 6
DB      2 KRRKR 6

RESULT 27
US-09-366-103-6
; Sequence 6, Application US/09366103
; Patent No. 6280944
; GENERAL INFORMATION:
; APPLICANT: Reichlin, Morris
; APPLICANT: Koren, Eugen
; TITLE OF INVENTION: Assay for Pathogenicity of Anti-DNA Antibodies
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street,
; STREET: Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,103
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,188
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRP145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 815-6508
; TELEFAX: (404) 815-6555
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-09-366-103-6

Query Match      83.3%; Score 25; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KRRKR 6
DB      2 KRRKR 7

RESULT 28
PCT-US91-08328-17
; Sequence 17, Application PC/TUS9108328
; GENERAL INFORMATION:
; APPLICANT: Ruggeri, Zaverio M.
; APPLICANT: Houghten, Richard A.
; TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
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; TITLE OF INVENTION: OF ADHESION MOLECULES
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08328
; FILING DATE: 19911107
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/610,363
; FILING DATE: 07-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Moroz, Eugene
; REGISTRATION NUMBER: 25,237
; REFERENCE/DOCKET NUMBER: 1198 4079PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Cross-links
; LOCATION: 4..11
; OTHER INFORMATION: /note= "Sequence linked by
; OTHER INFORMATION: interchain amide bond at Lys residue with Glu
; OTHER INFORMATION: residue on Arg3-Glu-Arg2-Ser-Arg-Gly-Asp-Val"
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 28-JUL-1987
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US Bi 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 03-JUL-1990
; PCT-US91-08328-17

Query Match 83.3%; Score 25; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 6
DB 3 RKRRR 8

RESULT 29
US-09-325-601-19
; Sequence 19, Application US/09325601
; Patent No. 6573045
; GENERAL INFORMATION:
; APPLICANT: Karn
; APPLICANT: Prescott
; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
; FILE REFERENCE: 3950/81235
; CURRENT APPLICATION NUMBER: US/09/325,601
; CURRENT FILING DATE: 1999-06-03

Query Match 83.3%; Score 25; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRK 5
DB 6 RKRRK 10

Search completed: April 13, 2006, 08:50:34
Job time : 47 secs

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
; OTHER INFORMATION: Q, R-pentapeptide library
US-09-325-601-19

Query Match 83.3%; Score 25; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRK 5
DB 6 RKRRK 10

RESULT 30
US-09-325-601-28
; Sequence 28, Application US/09325601
; Patent No. 6573045
; GENERAL INFORMATION:
; APPLICANT: Karn
; APPLICANT: Prescott
; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
; FILE REFERENCE: 3950/81235
; CURRENT APPLICATION NUMBER: US/09/325,601
; CURRENT FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Peptide from K,
; OTHER INFORMATION: Q, R-pentapeptide library
US-09-325-601-28

Query Match 83.3%; Score 25; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRK 5
DB 6 RKRRK 10

Search completed: April 13, 2006, 08:50:34
Job time : 47 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 13, 2006, 08:50:49 ; Search time 26 Seconds
(without alignments)
9.805 Million cell updates/sec

Title: US-09-816-688b-1
Perfect score: 30
Sequence: 1 KRKRK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 76596

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published Applications AA New:
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2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pep:
3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep:
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8: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	27	90.0	8	6 US-10-512-299A-45	Sequence 45, Appl
2	26	86.7	10	6 US-10-918-638-1	Sequence 1, Appli
3	26	86.7	10	6 US-10-246-300D-1	Sequence 1, Appli
4	26	86.7	20	7 US-11-223-699A-66	Sequence 66, Appl
5	26	86.7	20	7 US-11-121-566A-66	Sequence 66, Appl
6	25	83.3	5	7 US-11-179-639-21	Sequence 21, Appl
7	25	83.3	6	7 US-11-242-243-7	Sequence 7, Appli
8	25	83.3	6	7 US-11-242-243-8	Sequence 8, Appli
9	25	83.3	21	6 US-10-512-299A-55	Sequence 55, Appl
10	24	80.0	6	6 US-10-850-207-8	Sequence 8, Appli
11	24	80.0	7	6 US-10-923-112A-44	Sequence 44, Appl
12	24	80.0	7	7 US-11-041-103-5	Sequence 5, Appli
13	24	80.0	7	7 US-11-107-371-6	Sequence 6, Appli
14	24	80.0	7	7 US-11-141-725-10	Sequence 10, Appl
15	24	80.0	7	7 US-11-223-699A-12	Sequence 12, Appl
16	24	80.0	7	7 US-11-223-699A-64	Sequence 64, Appl
17	24	80.0	7	7 US-11-121-566A-12	Sequence 12, Appl
18	24	80.0	7	7 US-11-121-566A-64	Sequence 64, Appl
19	24	80.0	8	7 US-11-019-894A-26	Sequence 26, Appl
20	24	80.0	8	7 US-11-155-845-2	Sequence 2, Appli
21	24	80.0	8	7 US-11-075-648A-8	Sequence 8, Appli
22	24	80.0	9	6 US-10-595-426-7	Sequence 7, Appli
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24	24	80.0	9	6 US-10-512-299A-12	Sequence 12, Appl
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Sequence 30, Appl
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147     23 76.7 11 6 US-10-517-710-24
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150     23 76.7 11 7 US-11-045-024-3499

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Sequence 2, Appli
Sequence 7, Appli
Sequence 3499, Ap

Query Match      90.0%; Score 27; DB 6; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.8e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRRKR 6
       |||:|
Db      2 RRRRKR 7

RESULT 2
US-10-918-638-1
; Sequence 1, Application US/10918638
; Publication No. US20050249663A1
; GENERAL INFORMATION:
; APPLICANT: Copharos
; TITLE OF INVENTION: COBALAMIN MEDIATED DELIVERY OF NUCLEIC ACIDS, ANALOGS
; TITLE OF INVENTION: AND
; FILE REFERENCE: COP1010
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US/10/918,638
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: TAT nuclear localization signal peptide
US-10-918-638-1

Query Match      86.7%; Score 26; DB 6; Length 10;
Best Local Similarity 83.3%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRRKR 6
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Db      3 RRRRKR 8

RESULT 3
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; Sequence 1, Application US/10246300D
; Publication No. US20060074034A1
; GENERAL INFORMATION:
; APPLICANT: Copharos
; TITLE OF INVENTION: COBALAMIN MEDIATED DELIVERY OF NUCLEIC ACIDS, ANALOGS AND
; FILE REFERENCE: COP1010
; CURRENT FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: TAT nuclear localization signal peptide
US-10-246-300D-1

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Query Match 86.7%; Score 26; DB 6; Length 10;
Best Local Similarity 83.3%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRKR 6
Db 3 RRRQR 8

RESULT 4

US-11-223-699A-66
; Sequence 66, Application US/11223699A
; Publication No. US20060035815A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, LISHAN
; APPLICANT: CUI, KUNYUAN
; APPLICANT: HOUSTON JR., MICHAEL E.
; APPLICANT: MAYER, SASHA
; APPLICANT: CHEN, YUCHING
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR DELIVERY OF
; TITLE OF INVENTION: RIBONUCLEIC ACID TO A CELL
; FILE REFERENCE: 04-03CIP
; CURRENT APPLICATION NUMBER: US/11/223,699A
; CURRENT FILING DATE: 2005-09-08
; PRIOR APPLICATION NUMBER: 11/121,566
; PRIOR FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/667,833
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/656,572
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/613,416
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/570,513
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,512
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/568,027
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 66
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (11)
; OTHER INFORMATION: D-Gln
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (13)
; OTHER INFORMATION: D-Gln
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (15)
; OTHER INFORMATION: D-Gln
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (17)
; OTHER INFORMATION: D-Gln
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (19)
; OTHER INFORMATION: D-Gln
; OTHER INFORMATION: D-Gln

Query Match 86.7%; Score 26; DB 7; Length 20;
Best Local Similarity 83.3%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

US-11-223-699A-66

QY 1 RRRKR 6
Db 3 RRRQR 8

QY 1 RRRKR 6
Db 3 RRRQR 8

RESULT 5

US-11-121-566A-66
; Sequence 66, Application US/11121566A
; Publication No. US20060040882A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, LISHAN
; APPLICANT: CUI, KUNYUAN
; APPLICANT: CHEN, YUCHING
; APPLICANT: MAYER, SASHA
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DELIVERY OF
; TITLE OF INVENTION: NUCLEIC ACIDS INTO CELLS AND FOR MODIFYING EXPRESSION
; FILE REFERENCE: 04-03US
; CURRENT APPLICATION NUMBER: US/11/121,566A
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/667,833
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/656,572
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/613,416
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/570,513
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,512
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/568,027
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 66
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (11)
; OTHER INFORMATION: D-Gln
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (13)
; OTHER INFORMATION: D-Gln
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (15)
; OTHER INFORMATION: D-Gln
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (17)
; OTHER INFORMATION: D-Gln
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (19)
; OTHER INFORMATION: D-Gln
; OTHER INFORMATION: D-Gln

Query Match 86.7%; Score 26; DB 7; Length 20;
Best Local Similarity 83.3%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

US-11-121-566A-66

QY 1 RRRKR 6
Db 3 RRRQR 8

RESULT 6

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US-11-179-639-21
; Sequence 21, Application US/11179639
; Publication No. US20060034805A1
; GENERAL INFORMATION:
; APPLICANT: FANG, JIANMIN
; APPLICANT: JOOSS, KARIN
; TITLE OF INVENTION: AAV VECTOR COMPOSITIONS AND METHODS FOR ENHANCED
; FILE REFERENCE: 3802-101-11 US
; CURRENT APPLICATION NUMBER: US/11/179,639
; PRIOR FILING DATE: 2005-07-13
; PRIOR APPLICATION NUMBER: 60/587,082
; PRIOR FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: 60/659,871
; PRIOR FILING DATE: 2005-03-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-179-639-21

Query Match      83.3%; Score 25; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRKR 6
DB 1 KRRKR 5

RESULT 7
US-11-242-243-7
; Sequence 7, Application US/11242243
; Publication No. US20060024805A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baindur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/11/242,243
; PRIOR FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
US-11-242-243-7

Query Match      83.3%; Score 25; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRKR 6
DB 1 KRRKR 5

RESULT 8
US-11-242-243-8
; Sequence 8, Application US/11242243
; Publication No. US20060024805A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baindur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: DISINTEGRIN HOMOLOG
; FILE REFERENCE: 98-29
; CURRENT APPLICATION NUMBER: US/11/242,243
; PRIOR FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US/09/351,414
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide
US-11-242-243-8

Query Match      83.3%; Score 25; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRKR 6
DB 1 KRRKR 5

RESULT 9
US-10-512-299A-55
; Sequence 55, Application US/10512299A
; Publication No. US20060057668A1
; GENERAL INFORMATION:
; APPLICANT: TOAGOSEI CO., LTD.
; APPLICANT: YOSHIDA, Tetsuhiko
; APPLICANT: KUME, Msayoshi
; APPLICANT: YAMADA, Yoshinao
; APPLICANT: KOURAI, Hiroki
; TITLE OF INVENTION: ANTIMICROBIAL POLYPEPTIDE AND UTILIZATION THEREOF
; FILE REFERENCE: 54003.8003.US00
; CURRENT APPLICATION NUMBER: US/10/512,299A
; CURRENT FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: PCT/JP03/05225
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: JP 2002-124830
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-512-299A-55

Query Match      83.3%; Score 25; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRRRK 5
DB 5 KRRRK 9

RESULT 10
US-10-850-207-8
; Sequence 8, Application US/10850207
; Publication No. US20050283003A1
; GENERAL INFORMATION:
; APPLICANT: Spudich, James A.
; APPLICANT: Nock, Steffen
; APPLICANT: Wagner, Peter
```

; TITLE OF INVENTION: Reversible Immobilization of Arginine-Tagged Moieties on a Silica
; FILE REFERENCE: UCSD-04726
; CURRENT APPLICATION NUMBER: US/10/850,207
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US/09/486,480
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: PCT/US98/18531
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/057,929
; PRIOR FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-850-207-8

Query Match 80.0%; Score 24; DB 6; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
|:|:|:
DB 1 RRRRRR 6

RESULT 11
US-10-923-112A-44
; Sequence 44, Application US/10923112A
; Publication No. US2006004087A1
; GENERAL INFORMATION:
; APPLICANT: Kosak, Kenneth M.
; TITLE OF INVENTION: Chloroquine Coupled Nucleic Acids and Methods for Their Synthesis
; FILE REFERENCE: Confirmation No. 3293
; CURRENT APPLICATION NUMBER: US/10/923,112A
; CURRENT FILING DATE: 2004-08-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Table I Transduction Peptide
US-10-923-112A-44

Query Match 80.0%; Score 24; DB 6; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
|:|:|:
DB 1 RRRRRR 6

RESULT 12
US-11-041-103-5
; Sequence 5, Application US/11041103
; Publication No. US20050287548A1
; GENERAL INFORMATION:
; APPLICANT: Georgia Tech Research Corporation
; APPLICANT: Bao, Gang
; APPLICANT: Nitin, Nitin
; TITLE OF INVENTION: Activatable Probes and Methods For In Vivo Gene Detection
; FILE REFERENCE: 820701-1195
; CURRENT APPLICATION NUMBER: US/11/041,103
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: 10/179,730
; PRIOR FILING DATE: 2002-06-25

; TITLE OF INVENTION: Reversible Immobilization of Arginine-Tagged Moieties on a Silica
; FILE REFERENCE: UCSD-04726
; CURRENT APPLICATION NUMBER: US/10/850,207
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US/09/486,480
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: PCT/US98/18531
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/057,929
; PRIOR FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protein Transduction Domain
US-11-041-103-5

Query Match 80.0%; Score 24; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
|:|:|:
DB 1 RRRRRR 6

RESULT 13
US-11-107-371-6
; Sequence 6, Application US/11107371
; Publication No. US20060014289A1
; GENERAL INFORMATION:
; APPLICANT: AHMADIAN, MOHAMMAD
; APPLICANT: CUI, KUNYUAN
; APPLICANT: CHEN, LISHAN
; APPLICANT: HOUSTON JR., MICHAEL E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ENHANCING DELIVERY OF
; TITLE OF INVENTION: DOUBLE-STRANDED RNA OR A DOUBLE-STRANDED HYBRID NUCLEIC
; TITLE OF INVENTION: ACID TO REGULATE GENE EXPRESSION IN MAMMALIAN CELLS
; FILE REFERENCE: 04-0205
; CURRENT APPLICATION NUMBER: US/11/107,371
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/564,543
; PRIOR FILING DATE: 2004-04-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-107-371-6

Query Match 80.0%; Score 24; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
|:|:|:
DB 1 RRRRRR 6

RESULT 14
US-11-141-725-10
; Sequence 10, Application US/11141725
; Publication No. US20060014712A1
; GENERAL INFORMATION:
; APPLICANT: Neuman, Toomas
; TITLE OF INVENTION: Controlled Delivery of Therapeutic Compounds
; FILE REFERENCE: 34211/US/2 (473322-00024)

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; CURRENT APPLICATION NUMBER: US/11/141,725
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: US 60/575,660
; PRIOR FILING DATE: 2004-05-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-141-725-10

Query Match      80.0%; Score 24; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKRKR 6
        |.:|:|
Db      1 RRRRR 6

RESULT 15
US-11-223-699A-12
; Sequence 12, Application US/11223699A
; Publication No. US20060035815A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, LISHAN
; APPLICANT: CUI, KUNYUAN
; APPLICANT: HOUSTON JR., MICHAEL E.
; APPLICANT: MAYER, SASHA
; APPLICANT: CHEN, YUCHING
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR DELIVERY OF
; FILE REFERENCE: 04-03CIP
; CURRENT APPLICATION NUMBER: US/11/223,699A
; CURRENT FILING DATE: 2005-09-08
; PRIOR APPLICATION NUMBER: 11/121,566
; PRIOR FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/667,833
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/656,572
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/613,416
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/570,513
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,512
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/568,027
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: BrAc-Arg
US-11-223-699A-64

Query Match      80.0%; Score 24; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKRKR 6
        |.:|:|
Db      1 RRRRR 6

RESULT 17
US-11-121-566A-12
; Sequence 12, Application US/11121566A
; Publication No. US20060040882A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, LISHAN
; APPLICANT: CUI, KUNYUAN
; APPLICANT: CHEN, YUCHING
; APPLICANT: MAYER, SASHA
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DELIVERY OF
; TITLE OF INVENTION: NUCLEIC ACIDS INTO CELLS AND FOR MODIFYING EXPRESSION
; FILE REFERENCE: 04-03US
; CURRENT APPLICATION NUMBER: US/11/121,566A
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/667,833
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/656,572
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/613,416
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/570,513
; PRIOR FILING DATE: 2004-05-12
```

```
; Publication No. US20060035815A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, LISHAN
; APPLICANT: CUI, KUNYUAN
; APPLICANT: HOUSTON JR., MICHAEL E.
; APPLICANT: MAYER, SASHA
; APPLICANT: CHEN, YUCHING
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR DELIVERY OF
; FILE REFERENCE: 04-03CIP
; CURRENT APPLICATION NUMBER: US/11/223,699A
; CURRENT FILING DATE: 2005-09-08
; PRIOR APPLICATION NUMBER: 11/121,566
; PRIOR FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/667,833
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/656,572
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/613,416
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/570,513
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,512
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/568,027
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 64
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: BrAc-Arg
US-11-223-699A-64

Query Match      80.0%; Score 24; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKRKR 6
        |.:|:|
Db      1 RRRRR 6

RESULT 17
US-11-121-566A-12
; Sequence 12, Application US/11121566A
; Publication No. US20060040882A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, LISHAN
; APPLICANT: CUI, KUNYUAN
; APPLICANT: CHEN, YUCHING
; APPLICANT: MAYER, SASHA
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DELIVERY OF
; TITLE OF INVENTION: NUCLEIC ACIDS INTO CELLS AND FOR MODIFYING EXPRESSION
; FILE REFERENCE: 04-03US
; CURRENT APPLICATION NUMBER: US/11/121,566A
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/667,833
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/656,572
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/613,416
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/570,513
; PRIOR FILING DATE: 2004-05-12
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; PRIOR APPLICATION NUMBER: 60/570,512
 ; PRIOR FILING DATE: 2004-05-12
 ; PRIOR APPLICATION NUMBER: 60/568,027
 ; PRIOR FILING DATE: 2004-05-04
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO 12
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 US-11-121-566A-12

Query Match 80.0%; Score 24; DB 7; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.8e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 |.:|.:|
 Db 1 RRRRR 6

RESULT 18
 US-11-121-566A-64
 ; Sequence 64, Application US/11121566A
 ; Publication No. US2006004082A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHEN, LISHAN
 ; APPLICANT: CUI, KUNYUAN
 ; APPLICANT: CHEN, YUCHING
 ; APPLICANT: MAYER, SASHA
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DELIVERY OF
 ; TITLE OF INVENTION: NUCLEIC ACIDS INTO CELLS AND FOR MODIFYING EXPRESSION
 ; FILE REFERENCE: 04-03US
 ; CURRENT APPLICATION NUMBER: US/11/121,566A
 ; CURRENT FILING DATE: 2005-05-04
 ; PRIOR APPLICATION NUMBER: 60/667,833
 ; PRIOR FILING DATE: 2005-04-01
 ; PRIOR APPLICATION NUMBER: 60/656,572
 ; PRIOR FILING DATE: 2005-02-25
 ; PRIOR APPLICATION NUMBER: 60/613,416
 ; PRIOR FILING DATE: 2004-09-27
 ; PRIOR APPLICATION NUMBER: 60/570,513
 ; PRIOR FILING DATE: 2004-05-12
 ; PRIOR APPLICATION NUMBER: 60/570,512
 ; PRIOR FILING DATE: 2004-05-12
 ; PRIOR APPLICATION NUMBER: 60/568,027
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO 64
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)
 ; OTHER INFORMATION: BrAc-Arg
 US-11-121-566A-64

Query Match 80.0%; Score 24; DB 7; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.8e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 |.:|.:|
 Db 1 RRRRR 6

RESULT 19
 US-11-019-894A-26
 ; Sequence 26, Application US/11019894A
 ; Publication No. US20050245451A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pincus, Matthew R.
 ; TITLE OF INVENTION: PEPTIDES SELECTIVELY LETHAL TO THE MALIGNANT AND TRANSFORMED
 ; TITLE OF INVENTION: MAMMALIAN CELLS
 ; FILE REFERENCE: 1181-17 CIP A
 ; CURRENT APPLICATION NUMBER: US/11/019,894A
 ; CURRENT FILING DATE: 2004-12-21
 ; PRIOR APPLICATION NUMBER: 10/386,737
 ; PRIOR FILING DATE: 2003-03-12
 ; PRIOR APPLICATION NUMBER: 09/827,683
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/195,102
 ; PRIOR FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: 60/363,785
 ; PRIOR FILING DATE: 2002-03-12
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 26
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: peptide; Arg(8) membrane penetrating leader sequence
 US-11-019-894A-26

Query Match 80.0%; Score 24; DB 7; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.8e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
 |.:|.:|
 Db 1 RRRRR 6

RESULT 20
 US-11-155-845-2
 ; Sequence 2, Application US/11155845
 ; Publication No. US20050277193A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WICKHAM, THOMAS J.
 ; APPLICANT: KOVESDI, IMRE
 ; APPLICANT: BROUGH, DOUGLAS E.
 ; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
 ; FILE REFERENCE: 235922
 ; CURRENT APPLICATION NUMBER: US/11/155,845
 ; CURRENT FILING DATE: 2005-08-17
 ; PRIOR APPLICATION NUMBER: US 09/999,724
 ; PRIOR FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: US 09/101,751
 ; PRIOR FILING DATE: 1999-01-29
 ; PRIOR APPLICATION NUMBER: PCT/US96/191500
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 08/700,846
 ; PRIOR FILING DATE: 1996-08-21
 ; PRIOR APPLICATION NUMBER: US 08/701,124
 ; PRIOR FILING DATE: 1996-08-21
 ; PRIOR APPLICATION NUMBER: US 08/563,368
 ; PRIOR FILING DATE: 1995-11-28
 ; NUMBER OF SEQ ID NOS: 94
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 2
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-11-155-845-2

Query Match 80.0%; Score 24; DB 7; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRR 6
|:|:|:
Db 1 RRRRR 6

RESULT 21

US-11-075-648A-8
; Sequence 8, Application US/11075648A
; Publication No. US20060030535A1
; GENERAL INFORMATION:
; APPLICANT: Healy, Judith M.
; APPLICANT: Kurz, Markus
; APPLICANT: McCauley, Thomas Greene
; APPLICANT: Thompson, Kristin
; APPLICANT: Wilson, Charles
; APPLICANT: Margolskee, Dorothy J.
; TITLE OF INVENTION: Controlled Modulation of the Pharmacokinetics and Biodistribution
; FILE REFERENCE: 23239-575
; CURRENT APPLICATION NUMBER: US/11/075,648A
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/550,790
; PRIOR FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-11-075-648A-8

Query Match 80.0%; Score 24; DB 7; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRR 6
|:|:|:
Db 1 RRRRR 6

RESULT 22

US-10-985-426-7
; Sequence 7, Application US/10985426
; Publication No. US20050256069A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Rajeev, Kallanthottathil G.
; TITLE OF INVENTION: RNA AGENTS WITH BIOCLEAVABLE TETHERS
; FILE REFERENCE: 14174-099001
; CURRENT APPLICATION NUMBER: US/10/985,426
; CURRENT FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 10/916,185
; PRIOR FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US2004/011829
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/494,597

; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US 60/503,414
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/506,341
; PRIOR FILING DATE: 2003-09-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptide
US-10-985-426-7

Query Match 80.0%; Score 24; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRR 6
|:|:|:
Db 1 RRRRR 6

RESULT 23

US-10-509-787A-140
; Sequence 140, Application US/10509787A
; Publication No. US20050287602A1
; GENERAL INFORMATION:
; APPLICANT: O'DOWD, BRIAN P.
; APPLICANT: GEORGE, SUSAN R.
; TITLE OF INVENTION: METHOD OF IDENTIFYING TRANSMEMBRANE PROTEIN-INTERACTING COMPOUNDS
; FILE REFERENCE: 3477-110
; CURRENT APPLICATION NUMBER: US/10/509,787A
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: PCT/CA03/00542
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/442,556
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/422,891
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/387,570
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/379,419
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 60/371,704
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-509-787A-140

Query Match 80.0%; Score 24; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRR 6
|:|:|:
Db 2 KKKRR 7

RESULT 24

US-10-512-299A-12
; Sequence 12, Application US/10512299A
; Publication No. US20060057668A1
; GENERAL INFORMATION:
; APPLICANT: TOGOSSEI CO., LTD.

; APPLICANT: YOSHIDA, Tetsuhiko
; APPLICANT: KUME, Meayoshi
; APPLICANT: YAMADA, Yoshinao
; APPLICANT: KOURAI, Hiroki
; TITLE OF INVENTION: ANTIMICROBIAL POLYPEPTIDE AND UTILIZATION THEREOF
; FILE REFERENCE: 54003.8003.US00
; CURRENT APPLICATION NUMBER: US/10/512,299A
; CURRENT FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: PCT/JP03/05225
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: JP 2002-124830
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Drosophila sp.
US-10-512-299A-12

Query Match 80.0%; Score 24; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
:|:|:|
Db 2 KKRRKR 7

RESULT 25
US-11-016-542-20
; Sequence 20, Application US/11016542
; Publication No. US2005028239A1
; GENERAL INFORMATION:
; APPLICANT: ALLBRITTON, NANCY L.
; APPLICANT: SIMS, CHRISTOPHER E.
; APPLICANT: ROSSI, FRANCIS M.
; APPLICANT: SOUGHAYER, JOSEPH S.
; TITLE OF INVENTION: A CELL-PERMEABLE ENZYME ACTIVATION REPORTER THAT CAN BE
; TITLE OF INVENTION: LOADED IN A HIGH THROUGHPUT AND GENTLE MANNER
; FILE REFERENCE: CAL02-003-US
; CURRENT APPLICATION NUMBER: US/11/016,542
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: 60/530,875
; PRIOR FILING DATE: 2003-12-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-016-542-20

Query Match 80.0%; Score 24; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
:|:|:|
Db 1 RRRRRR 6

RESULT 26
US-11-133-804-47
; Sequence 47, Application US/11133804
; Publication No. US20060041105A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Tao
; APPLICANT: Olsen, Emilia S.
; APPLICANT: Whitney, Michael

; APPLICANT: Tsien, Roger Y.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Peptides Whose Uptake by Cells is Controllable
; FILE REFERENCE: 02307E-161520US
; CURRENT APPLICATION NUMBER: US/11/133,804
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US 10/699,562
; PRIOR FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: portion of compound (f) of Figure 17, R9, Arg9,
; OTHER INFORMATION: peptide portion B, uptake sequence
US-11-133-804-47

Query Match 80.0%; Score 24; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
:|:|:|
Db 1 RRRRRR 6

RESULT 27
US-11-200-703-7
; Sequence 7, Application US/11200703
; Publication No. US20060058266A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kesavan, Venkitesamy
; APPLICANT: Rajeev, Kallanthottathil G.
; TITLE OF INVENTION: CHEMICALLY MODIFIED OLIGONUCLEOTIDES
; FILE REFERENCE: 14174-089001
; CURRENT APPLICATION NUMBER: US/11/200,703
; CURRENT FILING DATE: 2005-08-10
; PRIOR APPLICATION NUMBER: 60/600,703
; PRIOR FILING DATE: 2004-08-10
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Exemplary Cell Permeation Peptide
US-11-200-703-7

Query Match 80.0%; Score 24; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
:|:|:|
Db 1 RRRRRR 6

RESULT 28
US-11-133-804-85
; Sequence 85, Application US/11133804
; Publication No. US20060041105A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Tao
; APPLICANT: Olsen, Emilia S.
; APPLICANT: Whitney, Michael
; APPLICANT: Tsien, Roger Y.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Peptides Whose Uptake by Cells is Controllable

```
; FILE REFERENCE: 02307E-161520US
; CURRENT APPLICATION NUMBER: US/11/133,804
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US 10/699,562
; PRIOR FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:basic portion B
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: Xaa = lysinamide attached through alpha and
; OTHER INFORMATION: epsilon nitrogen-bound cargo molecule
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: Xaa = dodecaheptyl-arginine
US-11-133-804-85
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Query Match      80.0%; Score 24; DB 7; Length 10;
Best Local Similarity 66.7%; Pred.No. 46;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RRRRRR 6
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Db 2 RRRRRR 7
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RESULT 29

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US-10-535-780-3
; Sequence 3, Application US/10535780
; Publication No. US20060026718A1
; GENERAL INFORMATION:
; APPLICANT: Werner, Stefan
; APPLICANT: Marillonnet, Sylvestre
; APPLICANT: Klimyuk, Victor
; APPLICANT: Gleba, Yuri
; TITLE OF INVENTION: Method of Controlling Cellular Processes in Plants
; FILE REFERENCE: 049202/289227
; CURRENT APPLICATION NUMBER: US/10/535,780
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: PCT/EP03/13018
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: DE 102 54 166.3
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Membrane Translocation Signal
US-10-535-780-3
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Query Match      80.0%; Score 24; DB 6; Length 11;
Best Local Similarity 66.7%; Pred.No. 50;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RRRRRR 6
   |::|:|
Db 1 RRRRRR 6
```

RESULT 30

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US-10-955-739-6
; Sequence 6, Application US/10955739
; Publication No. US20060067925A1
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; GENERAL INFORMATION:
; APPLICANT: Labhasetwar, Vinod D.
; APPLICANT: Reddy, Mazam K.
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR INHIBITING REPERFUSION INJURY IN THE
; FILE OF INVENTION: BRAIN
; FILE REFERENCE: NE-0016
; CURRENT APPLICATION NUMBER: US/10/955,739
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide targeting moiety.
US-10-955-739-6
```

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Query Match      80.0%; Score 24; DB 6; Length 11;
Best Local Similarity 66.7%; Pred.No. 50;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RRRRRR 6
   |::|:|
Db 3 RRRRRR 8
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Search completed: April 13, 2006, 08:53:54
Job time : 27 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2006, 08:45:30 ; Search time 38 Seconds
(without alignments)
15.192 Million cell updates/sec

Title: US-09-816-688B-1
Perfect score: 30
Sequence: 1 RRRRR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4071

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	83.3	21	2	I58423
2	22	73.3	10	2	A42089
3	22	73.3	18	2	PS0387
4	22	73.3	21	2	PN0082
5	21	70.0	16	2	A28144
6	20	66.7	19	2	B39845
7	20	66.7	21	2	B30146
8	20	66.7	21	2	JH0361
9	18	60.0	16	2	A35552
10	17	56.7	13	2	E39778
11	17	56.7	14	2	PL0040
12	17	56.7	19	2	A33361
13	17	56.7	20	2	I55663
14	17	56.7	21	2	I61306
15	16	53.3	8	2	I64832
16	16	53.3	9	2	S78762
17	16	53.3	10	2	PQ0785
18	16	53.3	16	2	A27803
19	16	53.3	16	2	S05703
20	16	53.3	18	2	S54270
21	16	53.3	19	4	I54264
22	16	53.3	20	2	S00315
23	16	53.3	20	2	S28405
24	15	50.0	14	2	S58426
25	15	50.0	15	2	S36888
26	15	50.0	15	2	S36891
27	15	50.0	17	1	A61339
28	15	50.0	18	2	S45373
29	15	50.0	20	2	I67551

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33	14	46.7	11	2	PH0913
34	14	46.7	12	2	A40763
35	14	46.7	12	2	S29859
36	14	46.7	13	2	JH0460
37	14	46.7	13	2	I51432
38	14	46.7	14	2	PC1215
39	14	46.7	14	2	C48401
40	14	46.7	15	2	PH0772
41	14	46.7	15	2	S36889
42	14	46.7	15	2	A32971
43	14	46.7	16	2	G45681
44	14	46.7	17	2	S61451
45	14	46.7	18	2	A40256
46	14	46.7	18	2	A61220
47	14	46.7	20	2	S17461
48	14	46.7	20	2	S68620
49	14	46.7	20	2	S78763
50	14	46.7	21	2	B35417
51	13	43.3	10	2	S71948
52	13	43.3	12	2	PH1605
53	13	43.3	13	2	S78519
54	13	43.3	13	2	S12388
55	13	43.3	13	2	S36887
56	13	43.3	14	2	S33803
57	13	43.3	14	2	JH0328
58	13	43.3	15	2	I49407
59	13	43.3	15	2	C41383
60	13	43.3	15	2	A61247
61	13	43.3	16	2	A45133
62	13	43.3	16	2	I52226
63	13	43.3	16	2	C37290
64	13	43.3	18	2	S02175
65	13	43.3	18	2	S39153
66	13	43.3	18	2	B48408
67	13	43.3	19	2	A38382
68	13	43.3	19	2	A48408
69	13	43.3	20	2	A60525
70	13	43.3	20	2	B38382
71	13	43.3	20	2	S11416
72	13	43.3	20	2	S32387
73	13	43.3	20	2	B35592
74	13	43.3	21	2	PC4381
75	12	40.0	4	2	I40870
76	12	40.0	7	2	B33541
77	12	40.0	8	2	A39892
78	12	40.0	8	2	PT0323
79	12	40.0	10	2	I52645
80	12	40.0	11	2	A26930
81	12	40.0	12	1	LFECPE
82	12	40.0	13	2	A53608
83	12	40.0	14	2	S23639
84	12	40.0	14	2	A41589
85	12	40.0	14	2	PA0045
86	12	40.0	15	2	A35417
87	12	40.0	15	2	S29175
88	12	40.0	16	2	S30384
89	12	40.0	16	2	S78415
90	12	40.0	16	2	E37290
91	12	40.0	17	2	A34835
92	12	40.0	17	2	A56885
93	12	40.0	17	2	A27636
94	12	40.0	17	2	A38824
95	12	40.0	17	2	JX0125
96	12	40.0	17	2	C84063
97	12	40.0	18	2	S56715
98	12	40.0	18	2	PH1621
99	12	40.0	18	2	JU0124
100	12	40.0	18	2	JU0125
101	12	40.0	19	2	PC1322
102	12	40.0	19	2	A49725

spectrin alpha chain
ribosomal protein
hypothetical prote
T-cell receptor be
sucrose-6-phosphat
gene p10 protein -
corticostatic pept
histone H4-1 precu
homeotic protein E
ribosomal protein
T-cell receptor be
ribosomal protein
heparin-binding le
orf 61.1 - phage T
hypothetical prote
interleukin-7 rece
epsilon receptor m
flavodoxin B - Azo
histone H4 - sea u
ribosomal protein
30K serine protein
matrix metalloprot
Ig H chain V-D-J r
ribosomal protein
argA protein - Sal
ribosomal protein
chaperone, TCPI-re
probrusin tetrade
placental calcium-
32K variable histo
urogenital tumor m
casein kinase II (
aldehyde dehydroge
homeotic protein G
acrosin (EC 3.4.21
translation elonga
21K high mobility
15K protein A - ka
21K high mobility
lysozyme (EC 3.2.1
15K protein B - ra
ribosomal protein
ribosomal protein
H+-exporting ATPase
dehydrin 7.5K poly
phospholipase C (5
hypothetical prote
P element, P cytot
Ig heavy chain CRD
gene B-50 protein
ermG leader peptid
pyrE leader peptid
neurotensin - guin
Ig kappa chain J s
25K elastin-bindin
porin por1 - Arabi
28K serine protein
D-galactose-bindin
hypothetical prote
ribosomal protein
homeotic protein G
monoclonal nonspec
cytotoxin B - Clos
tachyplesin I - ho
tachyplesin III -
hypothetical prote
hydroxymethylgluta
Ig H chain V-D-J r
polyphemusin I - A
polyphemusin II -
hypothetical prote
valine-tRNA ligase

103 12 40.0 19 2 S16332 peroxidase (EC 1.1
104 12 40.0 19 2 PC1324 hypothetical prote
105 12 40.0 19 2 JX0124 tachyplesin I prec
106 12 40.0 20 2 B33290 histone H2B - huma
107 12 40.0 20 2 A42267 J-kappa recombinat
108 12 40.0 21 2 I51224 somatotropin - chi
109 12 40.0 21 2 S34298 Ig-binding protein
110 12 40.0 21 2 C31182 hypothetical 2.4k
111 12 40.0 21 2 PQ0789 NADH2 dehydrogenas
112 12 40.0 21 2 T03773 probable histone H
113 11 36.7 6 2 B33932 Ig mu chain D regi
114 11 36.7 8 2 S70727 iggf protein - Shi
115 11 36.7 8 2 B54823 olfactory receptor
116 11 36.7 8 2 B54823 olfactory receptor
117 11 36.7 10 2 A54810 beta-neoendorphin
118 11 36.7 10 2 D54823 olfactory receptor
119 11 36.7 10 2 C54823 olfactory receptor
120 11 36.7 11 2 B43669 hypothetical prote
121 11 36.7 12 2 S01222 translation elonga
122 11 36.7 12 2 D28551 hypothetical prote
123 11 36.7 12 2 S10626 lipovitelin - Afr
124 11 36.7 12 2 T44420 hypothetical prote
125 11 36.7 13 1 UNBO neurotensin - bovi
126 11 36.7 13 1 UNQBT neurotensin - brus
127 11 36.7 13 2 A28505 neurotensin [valid
128 11 36.7 13 2 A61067 neurotensin - comm
129 11 36.7 13 2 PH1595 Ig H chain V-D-J r
130 11 36.7 13 2 G83988 hypothetical prote
131 11 36.7 14 2 B34135 DNA-binding protei
132 11 36.7 14 2 PH1617 Ig H chain V-D-J r
133 11 36.7 14 2 PH0762 T-cell receptor be
134 11 36.7 14 2 A37789 heat shock cognate
135 11 36.7 14 2 S45655 cathepsin L (EC 3.
136 11 36.7 14 2 G61308 hemocyanin chain 3
137 11 36.7 14 2 S68095 calcium-binding pr
138 11 36.7 14 2 H83778 hypothetical prote
139 11 36.7 15 2 S75841 T cell receptor V-
140 11 36.7 15 2 S02381 probable membrane
141 11 36.7 15 2 A17340 ribonucleoside-dip
142 11 36.7 16 2 PH1475 T-cell receptor be
143 11 36.7 16 2 A47393 neuropeptide calla
144 11 36.7 16 2 D98854 conserved hypothet
145 11 36.7 18 2 C30309 histone H4 - Euplo
146 11 36.7 18 2 P70239 Ig heavy chain CDR
147 11 36.7 18 2 B41589 40K elastin-bindin
148 11 36.7 18 2 A42016 mammary-derived gr
149 11 36.7 18 2 A20923 light meromyosin -
150 11 36.7 19 2 A44854 L-2,4-diaminobuty

ALIGNMENTS

RESULT 1
158423
arylhydrocarbon receptor - mouse
C:Species: Mus sp. (mouse)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: I58423
R;Minura, J.; Ema, M.; Sogawa, K.; Ikawa, S.; Fujii-Kuriyama, Y.
Pharmacogenetics 4, 349-354, 1994
A:Title: A complete structure of the mouse Ah receptor gene.
A:Reference number: I58423; MUID:95218835; PMID:7704041
A:Accession: I58423
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-21 <RES>
A:Cross-references: UNIPARC:UPI00000003C8; GB:S76844; NID:g913085; PIDN:AAB33978.1; PID:
C:Genetics:
A:Gene: Ah

Query Match 83.3%; Score 25; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRRRK 5
Db 12 RRRRK 16

RESULT 2
A42089
transcription factor I-POU protein, alternative splice form - fruit fly (Drosophila melar
C:Species: Drosophila melanogaster
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42089
R;Treacy, M.N.; Neilson, L.I.; Turner, E.E.; He, X.; Rosenfeld, M.G.
Cell 68, 491-505, 1992
A:Title: Twin of I-POU: a two amino acid difference in the I-POU homeodomain distinguishe
A:Reference number: A42089; MUID:92154665; PMID:1346754
A:Accession: A42089
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-10 <TRE>
A:Cross-references: UNIPROT:P24350; UNIPARC:UPI000016C02D; GB:S82271; NID:g945517; PID:g
C:Genetics:
A:Gene: FlyBase:Ipou
A:Cross-references: FlyBase:FBgn0004418

Query Match 73.3%; Score 22; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 KRRKR 6
Db 3 KRRKR 7

RESULT 3
PS0387
platelet-derived growth factor chain A2 - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-Sep-1993
C:Accession: PS0387
R;Nakahara, K.; Nishimura, H.; Kuro-O, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazaki, S
Biochem. Biophys. Res. Commun. 184, 811-818, 1992
A:Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vascul
A:Reference number: JN0248; MUID:92246970; PMID:1575749
A:Accession: PS0387
A:Molecule type: mRNA
A:Residues: 1-18 <NAK>
A:Cross-references: UNIPARC:UPI00001764FC
A:Note: this protein corresponds to the glioma type of human A chain
C:Superfamily: platelet-derived growth factor

Query Match 73.3%; Score 22; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 KRRKR 6
Db 8 KRRKR 12

RESULT 4
PN0082
sperm chromatin protein I2-2 - Argentinian shortfin squid (fragment)
C:Species: Illex argentinus (Argentinian shortfin squid)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: PN0082
R;Osadchuk, L.A.; Levina, N.B.; Telezhinskaya, I.N.; Khrapunov, S.N.; Berdyshev, G.D.; A
Bioorg. Khim. 16, 448-455, 1990
A:Title: Primary structure of main nuclear protein from headleg mollusk Illex argentinus
A:Reference number: PN0081; MUID:90329035; PMID:2375775
A:Accession: PN0082

A:Molecule type: protein
 A:Residues: 1-21 <OSA>
 A:Cross-references: UNIPROT:Q7M323; UNIPARC:UPI00001771FA
 A:Experimental source: sperm
 C:Superfamily: sperm histone
 C:Keywords: sperm

Query Match 73.3%; Score 22; DB 2; Length 21;
 Best Local Similarity 66.7%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 6
 :|||
 Db 2 RRRSR 7

RESULT 5
 A28144
 ribosomal protein S27a - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jul-2004
 C:Accession: A28144
 R:Redman, K.D.; Rechsteiner, M.
 J. Biol. Chem. 263, 4926-4931, 1988
 A:Title: Extended reading frame of a ubiquitin gene encodes a stable, conserved, basic p
 A:Reference number: A28144; MUID:88169619; PMID:2832412
 A:Accession: A28144
 A:Molecule type: protein
 A:Residues: 1-16 <RED>
 A:Cross-references: UNIPROT:Q97577; UNIPARC:UPI0000177161
 C:Superfamily: ubiquitin / rat ribosomal protein S27a; ribosomal protein S27a homology;
 C:Keywords: protein biosynthesis

Query Match 70.0%; Score 21; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 5.8e+02;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRK 6
 :|||
 Db 2 KRRKK 7

RESULT 6
 B39845
 PyrB leader peptide - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 05-Oct-2004
 C:Accession: B39845
 R:Quinn, C.L.; Stephenson, B.T.; Switzer, R.L.
 J. Biol. Chem. 266, 9113-9127, 1991
 A:Title: Functional organization and nucleotide sequence of the Bacillus subtilis pyrimi
 A:Reference number: A39845; MUID:91225016; PMID:1709162
 A:Accession: B39845
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-19 <QU>
 A:Cross-references: UNIPARC:UPI000017A35C; GB:M59757

Query Match 66.7%; Score 20; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRK 5
 :|||
 Db 2 KRRK 5

RESULT 7
 PS0146
 histone H1 - sea urchin (Hemicentrotus pulcherrimus) (fragment)
 C:Species: Hemicentrotus pulcherrimus
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
 C:Accession: PS0146

R:Suzuki, M.; Sugiura, M.; Ebashi, S.
 J. Biochem. 108, 347-355, 1990
 A:Title: Sea urchin protease specific to the SPKK motif in histone.
 A:Reference number: PS0145; MUID:9115778; PMID:2126010
 A:Accession: PS0146
 A:Molecule type: protein
 A:Residues: 1-21 <SUZ>
 A:Cross-references: UNIPROT:Q7M3M1; UNIPARC:UPI000017BF14
 C:Keywords: chromosomal protein; nucleosome

Query Match 66.7%; Score 20; DB 2; Length 21;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 5
 :|||
 Db 13 RSRRK 17

RESULT 8
 JH0361
 carassin - goldfish
 N:Alternate names: tachykinin-related peptide
 C:Species: Carassius auratus (goldfish)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
 C:Accession: JH0361
 R:Conlon, J.M.; O'Harte, F.; Peter, R.E.; Kah, O.
 J. Neurochem. 56, 1432-1436, 1991
 A:Title: Carassin: a tachykinin that is structurally related to neuropeptide-gamma from t
 A:Reference number: JH0361; MUID:91162221; PMID:2002352
 A:Accession: JH0361
 A:Molecule type: protein
 A:Residues: 1-21 <CON>
 A:Cross-references: UNIPROT:P25421; UNIPARC:UPI0000136FDE
 A:Experimental source: brain
 C:Keywords: amidated carboxyl end
 P:21/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 66.7%; Score 20; DB 2; Length 21;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 5
 :|||
 Db 9 RKRRK 13

RESULT 9
 A35552
 caldesmon - turkey (fragment)
 C:Species: Meleagris gallopavo (common turkey)
 C:Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 09-Jul-2004
 C:Accession: A35552
 R:Velaz, L.; Ingraham, R.H.; Chalovich, J.M.
 J. Biol. Chem. 265, 2929-2934, 1990
 A:Title: Dissociation of the effect of caldesmon on the ATPase activity and on the bindin
 A:Reference number: A35552; MUID:90153926; PMID:2137453
 A:Accession: A35552
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-16 <VEL>
 A:Cross-references: UNIPROT:Q7LZ12; UNIPARC:UPI000017C045

Query Match 60.0%; Score 18; DB 2; Length 16;
 Best Local Similarity 60.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRK 6
 :|||
 Db 10 RRQRK 14

RESULT 10

A:Reference number: I51892

A:Accession: I64832

A:Status: Preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-8 <RES>

A:Cross-references: UNIPROT:Q63139; UNIPARC:UPI00001708F8; GB:M99223; NID:G203644; PIDN:

C:Genetics:

A:Gene: SERCA1b

C:Keywords: hydrolase

Query Match 53.3%; Score 16; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRRK 5

DB 5 ERRK 8

RESULT 16

S78762

Ribosomal protein MRP-S12, mitochondrial - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: S78762

R:Graack, H.R.

submitted to the Protein Sequence Database, July 1999

A:Reference number: S78760

A:Accession: S78762

A:Molecule type: protein

A:Residues: 1-9 <GRA>

A:Cross-references: UNIPROT:Q7M375; UNIPARC:UPI000017C56E

C:Keywords: mitochondrial

F1-9/Product: ribosomal protein MRP-S12 (fragment) #status experimental <MAT>

Query Match

Best Local Similarity 53.3%; Score 16; DB 2; Length 9;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RKRRKR 6

DB 3 RKVRPR 8

RESULT 17

PQ0785

NADH2 dehydrogenase (EC 1.6.99.3) 27K chain - fava bean mitochondrion (fragment)

N:Alternate names: complex I 27K chain; NADH-ubiquinone reductase 27K chain

C:Species: mitochondrion Vicia faba (fava bean)

C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C:Accession: PQ0785

R:Letierme, S.; Boutry, M.

Plant Physiol. 102, 435-443, 1993

A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH:

A:Reference number: PQ0775; MUID:94151437; PMID:8108509

A:Accession: PQ0785

A:Molecule type: protein

A:Residues: 1-10 <LET>

A:Cross-references: UNIPROT:Q7M2G2; UNIPARC:UPI000017CDA9

C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the th

ranging from 5K to 75K.

C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by

C:Genetics:

A:Genome: mitochondrion

C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 53.3%; Score 16; DB 2; Length 10;

Best Local Similarity 60.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 5

DB 6 QKERK 10

RESULT 18

A27803

myosin light chain, smooth muscle - turkey (fragment)

C:Species: Meleagris gallopavo (common turkey)

C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 09-Jul-2004

C:Accession: A27803

R:Bengur, A.R.; Robinson, E.A.; Appella, E.; Sellers, J.R.

J. Biol. Chem. 262, 7613-7617, 1987

A:Title: Sequence of the sites phosphorylated by protein kinase C in the smooth muscle my

A:Reference number: A27803; MUID:87222380; PMID:3584131

A:Accession: A27803

A:Molecule type: protein

A:Residues: 1-16 <BEN>

A:Cross-references: UNIPROT:Q7LZ79; UNIPARC:UPI00001776E1

C:Superfamily: calmodulin; calmodulin repeat homology

C:Keywords: EF hand; muscle; smooth muscle

Query Match

Best Local Similarity 53.3%; Score 16; DB 2; Length 16;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6

DB 11 KKRPR 16

RESULT 19

S05703

homeotic protein ceh-2 - Caenorhabditis elegans (fragment)

C:Species: Caenorhabditis elegans

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-Oct-2004

C:Accession: S05703

R:Buerklin, T.R.; Finney, M.; Coulson, A.; Ruvkun, G.

Nature 341, 239-243, 1989

A:Title: Caenorhabditis elegans has scores of homeobox-containing genes.

A:Reference number: S05703; MUID:89384901; PMID:2571091

A:Accession: S05703

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-16 <BUE>

A:Cross-references: UNIPROT:O01962; UNIPARC:UPI000017A2EF

C:Genetics:

A:Gene: ceh-2

A:Map position: 1

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match

Best Local Similarity 53.3%; Score 16; DB 2; Length 16;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RKRRKR 6

DB 9 RTKHKR 14

RESULT 20

SS4270

GATA-2 protein - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C:Accession: SS4270

R:Brewer, A.C.; Guille, M.J.; Fear, D.J.; Partington, G.A.; Patient, R.K.

EMBO J. 14, 757-766, 1995

A:Title: Nuclear translocation of a maternal CCAAT factor at the start of gastrulation a

A:Reference number: SS4270; MUID:95188880; PMID:7882979

A:Accession: SS4270

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-18 <BRE>

A:Cross-references: UNIPROT:Q7LZS3; UNIPARC:UPI000017BF91

```
Query Match      53.3%; Score 16; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RKRR 4
        ||||
Db      9 RRR 12

RESULT 21
I54264
rhodopsin single base deletion frame shift mutant - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 08-Nov-1996 #text_change 20-Apr-2000
C:Accession: I54264
R:Horn, M.; Humphries, P.; Kunisch, M.; Marchese, C.; Apfelstedt-Sylla, E.; Fugl, L.; Z
Hum. Genet. 90 255-257, 1992
A:Title: Deletions in exon 5 of the human rhodopsin gene causing a shift in the reading
A:Reference number: I54264; MUID:93138610; PMID:1487240
A:Accession: I54264
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <HOR>
A:Cross-references: UNIPARC:UPI000011DDF9; GB:S55843; NID:g266287; PIDN:AAB25673.1; PID:
C:Genetics:
A:Gene: GDB:RHO
A:Cross-references: GDB:120347
A:Map position: 3q21.3-3q24

Query Match      53.3%; Score 16; DB 4; Length 19;
Best Local Similarity 60.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 KRRKR 6
        |||
Db      1 RRRAR 5

RESULT 22
S00315
photosystem I chain III - garden pea (fragment)
N:Alternate names: photosystem I 17K chain
C:Species: Pisum sativum (garden pea)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S00315; PT0018
R:Dunn, P.P.J.; Packman, L.C.; Pappin, D.; Gray, J.C.
PDBS Lett. 228 157-161, 1988
A:Title: N-terminal amino acid sequence analysis of the subunits of pea photosystem I.
A:Reference number: S00314; MUID:88137587; PMID:3277857
A:Accession: S00315
A:Molecule type: protein
A:Residues: 1-20 <DUN>
A:Cross-references: UNIPROT:P20119; UNIPARC:UPI0000132517
A>Note: 1-Ap was also found
C:Superfamily: photosystem I chain III
C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match      53.3%; Score 16; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 KRRKR 6
        |||
Db      16 KREKQ 20

RESULT 23
S28405
lamin B receptor - turkey (fragment)
N:Alternate names: inner nuclear membrane protein p58
C:Species: Meleagris gallopavo (common turkey)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S28405
```

```
R:Simos, G.; Georgatos, S.D.
EMBO J. 11, 4027-4036, 1992
A:Title: The inner nuclear membrane protein p58 associates in vivo with a p58 kinase and
A:Reference number: S28405; MUID:93010998; PMID:1327755
A:Accession: S28405
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <SIM>
A:Cross-references: UNIPROT:Q7LZ11; UNIPARC:UPI000017C046
C:Keywords: DNA binding; nucleus; receptor; transmembrane protein

Query Match      53.3%; Score 15; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 KRRK 5
        |||
Db      1 KQRK 4

RESULT 24
S58426
spermadhesin AWN homolog - horse (fragment)
C:Species: Equus caballus (domestic horse)
C>Date: 12-Feb-1998 #sequence_revision 15-May-1998 #text_change 07-May-1999
C:Accession: S58426
R:Calvete, J.J.; Mann, K.; Schaefer, W.; Sanz, L.; Reinert, M.; Nessau, S.; Raida, M.; T
Biochem. J. 310, 615-622, 1995
A:Title: Amino acid sequence of HSP-1, a major protein of stallion seminal plasma: effect
A:Reference number: S58424; MUID:95382782; PMID:7654203
A:Accession: S58426
A:Molecule type: protein
A:Residues: 1-14 <CAL>
A:Cross-references: UNIPARC:UPI000017C44B
A:Experimental source: seminal plasma

Query Match      50.0%; Score 15; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 RRKR 6
        |||
Db      4 RRRR 7

RESULT 25
S36888
ribosomal protein S12 - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S36888
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
PDBS Lett. 331, 9-14, 1993
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobact
A:Reference number: S36887; MUID:94009653; PMID:8405418
A:Accession: S36888
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <OHA>
A:Cross-references: UNIPROT:Q53538; UNIPARC:UPI000017729F
C:Superfamily: ribosomal protein S12
C:Keywords: protein biosynthesis; ribosome

Query Match      50.0%; Score 15; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RKRRK 5
        |||
Db      8 RKGRR 12

RESULT 26
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S36891
ribosomal protein - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S36891
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobacterium bovis
A:Reference number: S36887; MUID:94009653; PMID:8405418
A:Accession: S36891
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <OHA>
A:Cross-references: UNIPROT:Q9R545; UNIPARC:UPI00000BDC05

Query Match
Best Local Similarity 50.0%; Score 15; DB 2; Length 15;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RRRK 5
| | |
Db 10 RRRK 12

RESULT 27
A61339
vesiculakinin 1 - eastern yellowjacket
N:Contains: vesiculakinin 2
C:Species: Vespula maculifrons (eastern yellowjacket)
C>Date: 17-Jul-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: A61339
R:Yoshida, H.; Geller, R.G.; Pisano, J.J.
Biochemistry 15, 61-64, 1976
A:Title: Vesiculakinins: new carbohydrate-containing bradykinin derivatives.
A:Reference number: A61339; MUID:76114777; PMID:1247511
A:Accession: A61339
A:Molecule type: protein
A:Residues: 1-17 <YOS>
A:Cross-references: UNIPROT:P57672; UNIPARC:UPI0000138459
C:Superfamily: vesiculakinin
C:Keywords: antihypertensive; bradykinin; glycoprotein; venom
F1-17/Product: vesiculakinin 1 #status experimental <MAT1>
F3-17/Product: vesiculakinin 2 #status experimental <MAT2>
F19-17/Region: bradykinin-like
F3,4/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match
Best Local Similarity 50.0%; Score 15; DB 1; Length 17;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRKR 6
| | |
Db 5 RRRR 9

RESULT 28
S45373
translation elongation factor EF-1a - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S45373
R:Marty, I.; Brugidou, C.; Chartier, Y.; Meyer, Y.
Plant J. 4, 265-278, 1993
A:Title: Growth-related gene expression in Nicotiana tabacum mesophyll protoplasts.
A:Reference number: S45372; MUID:94035181; PMID:8220482
A:Accession: S45373
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-18 <MAR>
A:Cross-references: UNIPROT:Q40499; UNIPARC:UPI00000A6737; EMBL:Z14080; NID:G443955; PID:G443955

Query Match
Best Local Similarity 50.0%; Score 15; DB 2; Length 18;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRR 5
| | |
Db 14 QKKK 18

RESULT 29
I67551
monocyte chemotactic protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I67551
R:Steinbergen, E.J.; Verhagen, O.J.; van Leeuwen, E.F.; Behrendt, H.; Merle, P.A.; Westerling, J.; et al.
Eur. J. Immunol. 24, 900-908, 1994
A:Title: B precursor acute lymphoblastic leukemia third complementarity-determining region of the chemotactic protein (CCL20) gene.
A:Reference number: I53401; MUID:94200227; PMID:8149961
A:Accession: I67551
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-20 <RES>
A:Cross-references: UNIPARC:UPI0000116D84; GB:S69743; NID:G546304; PID:G546304
C:Genetics:
A:Gene: IGH VDJ

Query Match
Best Local Similarity 50.0%; Score 15; DB 2; Length 20;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRR 5
| | |
Db 2 RRRD 6

RESULT 30
PC7076
spectrin alpha chain, non-erythroid - mouse (fragment)
N:Alternate names: fodrin alpha chain
C:Species: Mus musculus (house mouse)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: PC7076
R:Tsuigita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.; et al.
Electrophoresis 21, 1853-1871, 2000
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of
A:Reference number: PC7072
A:Accession: PC7076
A:Molecule type: protein
A:Residues: 1-9 <TSU>
A:Cross-references: UNIPROT:P16546; UNIPARC:UPI000017C74E
A:Experimental source: strain C57BL/6Cr Slc, male; brain, striatum
C:Keywords: brain

Query Match
Best Local Similarity 46.7%; Score 14; DB 2; Length 9;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRR 4
| | |
Db 5 RKKK 8

Search completed: April 13, 2006, 08:49:44
Job time : 41 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 13, 2006, 08:42:09 ; Search time 227 Seconds
(without alignments)
18.648 Million cell updates/sec

Title: US-09-816-688B-1

Perfect score: 30

Sequence: 1 RRRKR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 15779

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	83.3	21	2	Q6LD79_MOUSE
2	25	83.3	21	2	Q6LECG_MOUSE
3	22	73.3	16	2	Q9UD21_HUMAN
4	22	73.3	20	2	Q9DEH9_XENLA
5	22	73.3	21	2	Q7M3Z3_ILIAR
6	21	70.0	15	2	Q5RF91_PONPY
7	21	70.0	15	2	Q35411_MOUSE
8	21	70.0	17	2	Q76N52_HUMAN
9	21	70.0	19	2	Q9UD87_HUMAN
10	21	70.0	19	2	Q8T0Y5_APIME
11	21	70.0	20	2	Q4ZG97_9DELA
12	21	70.0	20	2	Q4ZGB1_9DELA
13	21	70.0	20	2	Q4ZGB2_9DELA
14	21	70.0	21	2	Q9UC26_HUMAN
15	21	70.0	21	2	Q9UG23_9VIRU
16	21	70.0	21	2	Q9UG26_9VIRU
17	21	70.0	21	2	Q9JG30_9VIRU
18	20	66.7	10	2	Q8VN85_HELPY
19	20	66.7	14	2	Q4CX76_9CUCU
20	20	66.7	19	2	Q8HYW8_BOVIN
21	20	66.7	19	2	Q5PU92_BRARE
22	20	66.7	19	2	Q65MTO_9HIV1
23	20	66.7	20	2	Q4YAE2_PLABE
24	20	66.7	21	1	TKNC_CARAU
25	20	66.7	21	2	Q7M3M1_HEMPU
26	20	66.7	21	2	Q662J7_BORGA
27	20	66.7	21	2	Q9DD39_NIPNI
28	20	66.7	21	2	Q9PRZ3_ONCMY
29	19	63.3	10	2	Q70Y78_PLECTRANTHU
30	19	63.3	11	2	Q70Y85_PLATOSTOMA
31	19	63.3	13	2	Q65331_NPVAC

32	19	63.3	14	2	Q70Y82_9LAMI	Q70Y82 plectranthu
33	19	63.3	15	2	Q5XPT1_SOLTU	Q5XPT1 solanum tub
34	19	63.3	15	2	Q5PX33_9CHLO	Q5PX33 halimeda tu
35	19	63.3	15	2	Q7WR21_9FLAO	Q7WR21 flavobacter
36	19	63.3	17	2	Q5PX35_9CHLO	Q5PX35 halimeda tu
37	19	63.3	18	2	Q16173_HUMAN	Q16173 homo sapien
38	19	63.3	19	2	Q9UH46_HUMAN	Q9UH46 homo sapien
39	19	63.3	19	2	Q70Y86_9LAMI	Q70Y86 platostoma
40	19	63.3	20	2	Q7S325_NEUCR	Q7S325 neurospora
41	19	63.3	20	2	Q6UQN2_9PASS	Q6UQN2 anomalospliz
42	19	63.3	20	2	Q6UQN3_9PASS	Q6UQN3 vidua orien
43	19	63.3	20	2	Q6UQN4_9PASS	Q6UQN4 vidua parad
44	19	63.3	20	2	Q6UQN5_9PASS	Q6UQN5 vidua obtus
45	19	63.3	20	2	Q6UQN6_9PASS	Q6UQN6 vidua hypoc
46	19	63.3	20	2	Q6UQN8_9PASS	Q6UQN8 vidua macro
47	19	63.3	20	2	Q6UQN9_9PASS	Q6UQN9 vidua wileo
48	19	63.3	20	2	Q6UQP0_9PASS	Q6UQP0 vidua camer
49	19	63.3	20	2	Q6UQP2_9PASS	Q6UQP2 vidua rari
50	19	63.3	20	2	Q6UQP3_9PASS	Q6UQP3 vidua purpu
51	19	63.3	20	2	Q6UQP4_9PASS	Q6UQP4 vidua regia
52	19	63.3	20	2	Q6UQP5_9PASS	Q6UQP5 vidua fisch
53	19	63.3	21	2	Q4XNU6_PLACH	Q4XNU6 plasmodium
54	18	60.0	11	2	Q8R2J7_MESAU	Q8R2J7 mesocricetu
55	18	60.0	13	2	Q9R8R9_STRPY	Q9R8R9 streptococ
56	18	60.0	15	2	Q6LC05_PSEAE	Q6LC05 pseudomonas
57	18	60.0	16	2	Q7LZ12_MELGA	Q7LZ12 meleagris g
58	18	60.0	17	2	P79167_HORSE	P79167 equus cabal
59	18	60.0	17	2	Q5KC74_EUGGL	Q5KC74 eucalyptus
60	18	60.0	18	2	Q7RNN4_PLAYO	Q7RNN4 plasmodium
61	18	60.0	19	2	Q4XDU3_PLACH	Q4XDU3 plasmodium
62	18	60.0	19	2	Q4Y054_PLACH	Q4Y054 plasmodium
63	18	60.0	19	2	Q4V6H4_PLACH	Q4V6H4 plasmodium
64	18	60.0	19	2	Q905G8_9HIV1	Q905G8 human immun
65	18	60.0	19	2	Q905I8_9HIV1	Q905I8 human immun
66	18	60.0	19	2	Q905J6_9HIV1	Q905J6 human immun
67	18	60.0	19	2	Q90RF8_9HIV1	Q90RF8 human immun
68	18	60.0	20	2	Q9UCM1_HUMAN	Q9UCM1 homo sapien
69	18	60.0	20	2	Q7RKX5_PLAYO	Q7RKX5 plasmodium
70	17	56.7	7	2	P92210_AGRCR	P92210 agropyron c
71	17	56.7	7	2	P92214_9FOAL	P92214 amblyopyrum
72	17	56.7	7	2	P92218_9FOAL	P92218 australopyr
73	17	56.7	7	2	P92221_BROIN	P92221 bromus iner
74	17	56.7	7	2	P92226_CRIDE	P92226 crithopsis
75	17	56.7	7	2	P92372_9FOAL	P92372 haynaldia v
76	17	56.7	7	2	P92381_9FOAL	P92381 hordeum bra
77	17	56.7	7	2	P92385_HORMA	P92385 hordeum mar
78	17	56.7	7	2	P92387_9FOAL	P92387 henrardia p
79	17	56.7	7	2	P92390_HETPI	P92390 heteranthe
80	17	56.7	7	2	P92393_HORVU	P92393 hordeum vul
81	17	56.7	7	2	P92403_LOPEL	P92403 lophopyrum
82	17	56.7	7	2	P92421_PSAFR	P92421 psathyrosta
83	17	56.7	7	2	P92425_PSEPI	P92425 pseudoroegn
84	17	56.7	7	2	P92427_9FOAL	P92427 peridictyon
85	17	56.7	7	2	P92430_AEGTA	P92430 aegilops ta
86	17	56.7	7	2	P92440_THIBE	P92440 thinnopyrum
87	17	56.7	7	2	P92442_TARCM	P92442 taeniatheru
88	17	56.7	7	2	Q9YIQ9_ADE04	Q9YIQ9 human adeno
89	17	56.7	7	2	Q9YIRO_ADE07	Q9YIRO human adeno
90	17	56.7	7	2	Q9YIY3_ADE07	Q9YIY3 human adeno
91	17	56.7	8	2	Q84271_HPV19	Q84271 human papil
92	17	56.7	8	2	Q84273_HPV25	Q84273 human papil
93	17	56.7	9	2	Q45852_CLOBU	Q45852 clostridium
94	17	56.7	12	2	Q5EFZ2_9BRYO	Q5EFZ2 buxbaumia a
95	17	56.7	13	2	Q9UM89_HUMAN	Q9UM89 homo sapien
96	17	56.7	13	2	Q60F86_9BRYO	Q60F86 sphagnum gi
97	17	56.7	13	2	Q60F89_TAKLE	Q60F89 takakia lep
98	17	56.7	14	2	Q7S9F5_NEUCR	Q7S9F5 neurospora
99	17	56.7	14	2	Q7M385_PIG	Q7M385 sus scrofa
100	17	56.7	15	2	Q15344_HUMAN	Q15344 homo sapien
101	17	56.7	16	2	Q9UD47_HUMAN	Q9UD47 homo sapien
102	17	56.7	16	2	Q9UD47_HUMAN	Q9UD47 homo sapien
103	17	56.7	18	2	Q5RL96_HUMAN	Q5RL96 homo sapien
104	17	56.7	18	2	Q4YAA7_PLABE	Q4YAA7 plasmodium


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RT transition.";
RL Mol. Cell. Biol. 15:2612-2624 (1995).
SQ SEQUENCE 16 AA; 2089 MW; 777EFC69C445E29C CRC64;

Query Match
Best Local Similarity 73.3%; Score 22; DB 2; Length 16;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRKR 6
DB 3 RRRER 8

RESULT 4
Q9DEH9 XENLA
ID Q9DEH9_XENLA PRELIMINARY; PRT; 20 AA.
AC Q9DEH9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE MCMA (Fragment).
GN Name=Mcma4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=J; TISSUE=Spleen;
RA MEDLINE=20456723; PubMed=11003390; DOI=10.1007/s002510000227;
RX Fujimori A., Araki R., Fukumura R., Ohhata T., Takahashi H.,
RA Kawahara A., Tatsumi K., Abe M.;
RT "Identification of four highly conserved regions in DNA-PKcs.";
RL Immunogenetics 51:965-973 (2000).
DR EMBL; AB016729; BAB19264.1; -; Genomic_DNA.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2247 MW; 7F3A0A50B30441AB CRC64;

Query Match
Best Local Similarity 73.3%; Score 22; DB 2; Length 20;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRRKR 6
DB 10 RRRKR 15

RESULT 5
Q7M3Z3 ILLAR
ID Q7M3Z3_ILLAR PRELIMINARY; PRT; 21 AA.
AC Q7M3Z3;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Sperm chromatin protein 12-2 (Fragment).
OS Illex argentinus (Argentinian squid).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Oegopsida; Ommastrephidae; Illex.
OX NCBI_TaxID=6628;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90329035; PubMed=2375775;
RA Osadchuk L.A., Levina N.B., Telezhinskaya I.N., Khrapunov S.N.,
RA Berdysher G.D., Aldanova N.A.;
RT "Primary structure of main nuclear protein from headleg mollusk Illex
RT argentinus and comparison with sperm protein of other animals.";
RL Biorg. Khim. 16:448-455 (1990).
DR FIR; FN0082; FN0082.
FT NON_TER 1 1
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2931 MW; A9F8D98969174878 CRC64;

Query Match
Best Local Similarity 73.3%; Score 22; DB 2; Length 21;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRRKR 6
DB 2 RRRSR 7

RESULT 6
Q9RF91 PONPY
ID Q9RF91_PONPY PRELIMINARY; PRT; 15 AA.
AC Q9RF91;
DT 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE Hypothetical protein DKFZp469P2021.
GN Name=DKFZp469P2021;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; CR857270; CAH89566.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 15 AA; 1788 MW; 530A15F11C204E3A CRC64;

Query Match
Best Local Similarity 70.0%; Score 21; DB 2; Length 15;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRRKR 6
DB 8 RRRKQ 12

RESULT 7
O35411 MOUSE
ID O35411_MOUSE PRELIMINARY; PRT; 15 AA.
AC O35411;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Beta III spectrin (Fragment).
GN Name=Spnb3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole embryo;
RX MEDLINE=99045654; PubMed=9826670; DOI=10.1073/pnas.95.24.14158;
RA Stankewich M.C., Tee W.T., Peters L.L., Ch'ng Y., John K.M.,
RA Stabach P.R., Devarsjan P., Morrow J.S., Lux S.E.;
RT "A widely expressed betaIII spectrin associated with Golgi and
RT cytoplasmic vesicles.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:14158-14163 (1998).
DR EMBL; AF026489; AAC79505.1; -; mRNA.
DR MGI; MGI:1313261; Spnb3.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 2029 MW; CAF6B165F69F1AA8 CRC64;

Query Match
Best Local Similarity 70.0%; Score 21; DB 2; Length 15;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 2 REREKR 7

RESULT 8
Q76N52 HUMAN
ID Q76N52 HUMAN PRELIMINARY; PRT; 17 AA.
AC Q76N52;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Ribosomal protein L41 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98248690; PubMed=9582194;
RA Kenmochi N., Kawaguchi T., Rozen S., Davis E., Goodman N.,
RA Hudson T.J., Tanaka T., Page D.C.;
RT "A map of 75 human ribosomal protein genes.";
RL Genome Res. 8:509-523(1998).
DR EMBL; AB007186; BAA28285.1; -; Genomic DNA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2385 MW; 1990BBE3EEA7E344 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 6 RKRRMR 11

RESULT 9
Q9UDB7 HUMAN
ID Q9UDB7 HUMAN PRELIMINARY; PRT; 19 AA.
AC Q9UDB7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE CD8 BETA chain isoform S BETA1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93170376; PubMed=8436166;
RA DiSanto J.P., Smith D., de Bruin D., Lacy E., Flomenberg N.;
RT "Transcriptional diversity at the duplicated human CD8 beta loci.";
RL Eur. J. Immunol. 23:320-326(1993).
SQ SEQUENCE 19 AA; 2527 MW; D1405FE2CEEB4419 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 5 RRRRAR 10

RESULT 10
Q8TOY5 APIME
ID Q8TOY5 APIME PRELIMINARY; PRT; 19 AA.
AC Q8TOY5;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE UORP.
GN Name=Dop2;
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98194783; PubMed=9535160;
RA Ebert P.R., Rowland J.E., Toma D.P.;
RT "Isolation of seven unique biogenic amine receptor clones from the
RT honey bee by library scanning.";
RL Insect Mol. Biol. 7:151-162(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Brain mushroom bodies;
RX MEDLINE=22602973; PubMed=12717701; DOI=10.1002/neu.10209;
RA Humphries M.A., Mustard J.A., Hunter S.J., Mercer A., Ward V.,
RA Ebert P.R.;
RT "Invertebrate D2 type dopamine receptor exhibits age-based plasticity
RT of expression in the mushroom bodies of the honeybee brain.";
RL J. Neurobiol. 55:315-330(2003).
DR EMBL; AF498306; AAM19333.1; -; mRNA.
SQ SEQUENCE 19 AA; 2150 MW; 3EB6B90996DFCC16 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 5 RMRRKK 10

RESULT 11
Q4ZG97_9DELA
ID Q4ZG97_9DELA PRELIMINARY; PRT; 20 AA.
AC Q4ZG97;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Rex (Fragment).
GN Name=rex;
OS Human T-lymphotropic virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C4 HC;
RA Sabouri A.H., Saito M., Tatsumi R., Hanada K., Usuku K., Furukawa Y.,
RA Izumo S., Arimura K., Fujisawa J., Farid R., Osame M.;
RT "Functional and Phylogenetic Analysis of Human T-cell Lymphotropic
RT Virus Type 1 (HTLV-1) tax Subtypes.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB211219; BAD95666.1; -; Genomic DNA.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2588 MW; CCE8286F1913DEF9 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
Db 1 RKRRKR 6
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```
Db 10 RSQRKR 15

RESULT 12
Q4ZGB1_9DELA PRELIMINARY; PRT; 20 AA.
AC Q4ZGB1;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Rex (Fragment).
GN Name=rex;
OS Human T-lymphotropic virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C7 HC;
RA Sabouri A.H., Saïto M., Tatsumi R., Hanada K., Usuku K., Furukawa Y.,
RA Izumo S., Arimura K., Fujisawa J., Farid R., Osame M.;
RT "Functional and Phylogenetic Analysis of Human T-cell Lymphotropic
RT Virus type 1 (HTLV-1) tax Subtypes.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB211200; BAD95652.1; -; Genomic_DNA.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2588 MW; CCE8286F1913DEF9 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
| : |||
Db 10 RSQRKR 15

RESULT 13
Q4ZGB2_9DELA PRELIMINARY; PRT; 20 AA.
AC Q4ZGB2;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Rex (Fragment).
GN Name=rex;
OS Human T-lymphotropic virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B2 HAM;
RA Sabouri A.H., Saïto M., Tatsumi R., Hanada K., Usuku K., Furukawa Y.,
RA Izumo S., Arimura K., Fujisawa J., Farid R., Osame M.;
RT "Functional and Phylogenetic Analysis of Human T-cell Lymphotropic
RT Virus type 1 (HTLV-1) tax Subtypes.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB211199; BAD95651.1; -; Genomic_DNA.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2588 MW; CCE8286F1913DEF9 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
| : |||
Db 10 RSQRKR 15

RESULT 14
Q9UC26_HUMAN PRELIMINARY; PRT; 21 AA.
AC Q9UC26;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Stromelysin-3 zymogen (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95265105; PubMed=7746327; DOI=10.1038/375244a0;
RA Pei D., Weiss S.J.;
RT "Furin-dependent intracellular activation of the human stromelysin-3
RT zymogen.";
RL Nature 375:244-247(1995).
SQ SEQUENCE 21 AA; 2300 MW; BE8C224E96D4B9D6 CRC64;

Query Match 70.0%; Score 21; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
| : |||
Db 12 RNRQKR 17

RESULT 15
Q9JG23_9VIRU PRELIMINARY; PRT; 21 AA.
AC Q9JG23;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE ORF1 (Fragment).
GN Name=ORF1;
OS Torque teno virus.
OC Viruses; ssDNA viruses; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20261737; PubMed=10799591;
RX DOI=10.1128/JVI.74.11.5161-5167.2000;
RA Tanaka T., Miyakawa Y., Mayumi M.;
RA Okamoto H., Ukita M., Nishizawa T., Kishimoto J., Hoshi Y., Mizuo H.,
RT "Circular double-stranded forms of TT virus DNA in the liver.";
RL J. Virol. 74:5161-5167(2000).
DR EMBL; AB040786; BAA94205.1; -; Genomic_DNA.
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 3001 MW; 969C86599D8A344B CRC64;

Query Match 70.0%; Score 21; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
| : |||
Db 8 RTRRRR 13

RESULT 16
Q9JG26_9VIRU PRELIMINARY; PRT; 21 AA.
AC Q9JG26;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE ORF1 (Fragment).
GN Name=ORF1;
OS Torque teno virus.
```

```
OC Viruses; ssDNA viruses; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20261737; PubMed=10799591;
RY DOI=10.1128/JVI.74.11.5161-5167.2000;
RA Okamoto H., Ukita M., Nishizawa T., Kishimoto J., Hoshi Y., Mizuo H.,
RA Tanaka T., Miyakawa Y., Mayumi M.;
RT "Circular double-stranded forms of TT virus DNA in the liver.";
RL J. Virol. 74:5161-5167(2000).
DR EMBL; AB040782; BAA94202.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 21
SQ SEQUENCE 21 AA; 2922 MW; 953F86599D8A344B CRC64;

Query Match 70.0%; Score 21; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
DB 8 RTRRRR 13

RESULT 17
Q9UG30_9VIRU PRELIMINARY; PRT; 21 AA.
AC Q9UG30;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE ORF1 (Fragment).
GN Name=ORF1;
OS Torque teno virus.
OC Viruses; ssDNA viruses; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20261737; PubMed=10799591;
RY DOI=10.1128/JVI.74.11.5161-5167.2000;
RA Okamoto H., Ukita M., Nishizawa T., Kishimoto J., Hoshi Y., Mizuo H.,
RA Tanaka T., Miyakawa Y., Mayumi M.;
RT "Circular double-stranded forms of TT virus DNA in the liver.";
RL J. Virol. 74:5161-5167(2000).
DR EMBL; AB040778; BAA94198.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 21
SQ SEQUENCE 21 AA; 3001 MW; 969C86599D8A344B CRC64;

Query Match 70.0%; Score 21; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
DB 8 RTRRRR 13

RESULT 18
Q8VN85_HELPHY PRELIMINARY; PRT; 10 AA.
AC Q8VN85;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DE 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Urease accessory protein.
GN Name=ureF;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NQ267;
RX MEDLINE=21625040; PubMed=11742075; DOI=10.1073/pnas.251396098;
RA Falush D., Kraft C., Taylor N.S., Correa P., Fox J.G., Achtman M.,
RA Suerbaum S.;
RT "Recombination and mutation during long-term gastric colonization by
RT Helicobacter pylori: estimates of clock rates, recombination size and
RT minimal age.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:15056-15061(2001).
DR EMBL; AJ418329; CAD11229.1; -; Genomic_DNA.
SQ SEQUENCE 10 AA; 1329 MW; 81E8020403332411 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRRKR 6
DB 4 RKREK 9

RESULT 19
Q4GX76_9CUCU PRELIMINARY; PRT; 14 AA.
AC Q4GX76;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Ribosomal protein L4le (Fragment).
GN Name=rpl4le;
OS Curculio glandium.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Curculionidae; Curculioninae; Curculionini; Curculio.
OX NCBI_TaxID=197013;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Longhorn S.J., Vogler A.P.;
RT "Ribosomal proteins of Coleoptera.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AM049147; CAJ17447.1; -; mRNA.
KW Ribosomal protein.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1912 MW; 53EBA7E350113A33 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRKR 6
DB 6 RKRRVR 11

RESULT 20
Q8HYW9_BOVIN PRELIMINARY; PRT; 19 AA.
AC Q8HYW9;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Calcium channel alpha-2/delta subunit 1 (Fragment).
GN Name=cacna2d1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Hostein-Friesian; TISSUE=Leukocyte;
RA Buittkamp J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ439531; CAD28621.1; -; Genomic_DNA.
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FT NON TER 1 1
FT NON TER 19 19
SQ SEQUENCE 19 AA; 2143 MW; 4B078FAL355E79E1 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRR 4
DB 12 RKRR 15

RESULT 21
QSPU92_BRARE PRELIMINARY; PRT; 19 AA.
AC QSPU92;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE T-cell factor 7 isoform D (Fragment).
GN Name=tcf7;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB;
RX PubMed=15765502; DOI=10.1002/dvdy.20330;
RA Veien E.S., Grierson M.J., Saund R.S., Dorsky R.I.;
RT "Expression pattern of zebrafish tcf7 suggests unexplored domains of
RT Wnt/beta-catenin activity.";
RL Dev. Dyn. 233:233-239(2005).
DR EMBL; AY825027; AAV84017.1; -; mRNA.
DR ZFIN; ZDB-GENE-050222-4; tcf7.
FT NON TER 1
SQ SEQUENCE 19 AA; 2239 MW; 30C5948AC4B9B9A2 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RKRR 6
DB 1 RKRR 4

RESULT 22
Q66MT0_9HIV1 PRELIMINARY; PRT; 19 AA.
AC Q66MT0;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Vpr protein (Fragment).
GN Name=vpr;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Herring B.L., Grant R.M., Delwart E.L.;
RT "No superinfection among seroconcordant couples after well-defined
RT exposure.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY686105; AAU5411.1; -; Genomic_RNA.
FT NON TER 1
SQ SEQUENCE 19 AA; 2209 MW; D23D5538822A2ED0 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 19;

Best Local Similarity 66.7%; Pred. No. 3.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRR 6
DB 8 RQRTR 13

RESULT 23
Q4YAE2_PLABE PRELIMINARY; PRT; 20 AA.
AC Q4YAE2;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB401699.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA01007113; CAI05279.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 20 AA; 2358 MW; 75EAD8B63E5C6C5A CRC64;

Query Match 66.7%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKRR 5
DB 6 RKRR 9

RESULT 24
TKNC_CARAU STANDARD; PRT; 21 AA.
AC P25421;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carassin.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91162221; PubMed=2002352;
RA Conlon J.M., O'Harte F., Peter R.E., Kah O.;
RT "Carassin: a tachykinin that is structurally related to neuropeptide-
RT gamma from the brain of the goldfish.";
RL J. Neurochem. 56:1432-1436(1991).
CC -! FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.

```

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CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; JH0361; JH0361.
DR InterPro: IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.
FT MOD RES 21 21 Methionine amide.
SQ SEQUENCE 21 AA; 2369 MW; 1460DC6C5B097A29 CRC64;

Query Match 66.7%; Score 20; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRRRK 5
Db 9 RRRRK 13

RESULT 25
Q7M3M1 HEMPU
ID Q7M3M1 HEMPU PRELIMINARY; PRT; 21 AA.
AC Q7M3M1
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Histone H1 (Fragment).
OS Hemicotrotus pulcherrimus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoides; Euechinoides; Echinacea; Echinoida; Strongylocentrotidae;
OC Hemicotrotus.
ON NCBI_TaxID=7650;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=91115778; PubMed=2126010;
RA Suzuki M., Sugiura M., Ebashi S.;
RT "Sea urchin protease specific to the SPKK motif in histone.";
RL J. Biochem. 108:347-355(1990).
FT PIR; PS0146; PS0146.
FT NON_TER 1 1
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2378 MW; 0B32BA52D8DD06D7 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 21;
Best Local Similarity 80.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRRRK 5
Db 13 RRRRK 17

RESULT 26
Q662J7 BORG
ID Q662J7 BORG PRELIMINARY; PRT; 21 AA.
AC Q662J7
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BG0166;
OS Borrelia garinii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
OC Borrelia burgdorferi group.
ON NCBI_TaxID=29519;
RN [1]
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PBI;
RA Gloeckner G., Lehmann R., Romualdi A., Pradella S.,
RA Schulte-Spechtel U., Wilske B., Suehnel J., Platzer M.;
RT "Comparative analysis of the Borrelia garinii genome.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000013; AAU07024.1; -; Genomic_DNA.
SQ SEQUENCE 21 AA; 2526 MW; 7FCA6CC18506B3D3 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRK 6
Db 10 QKKKKR 15

RESULT 27
Q9DD39 NIPNI
ID Q9DD39 NIPNI PRELIMINARY; PRT; 21 AA.
AC Q9DD39
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE Non-W chromodomain helicase DNA binding protein (W-linked chromodomain
DE helicase DNA binding protein) (Fragment).
GN Name=non-W CHD; Synonyms=W-linked CHD;
OS Nipponia nippon (Crested ibis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Ciconiiformes; Threskiornithidae;
OC Nipponia.
ON NCBI_TaxID=128390;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Arai Y., Ishii S., Kikuchi M.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049444; BAB15805.1; -; Genomic DNA.
DR EMBL; AB049443; BAB15804.1; -; Genomic DNA.
GO GO:0004386; F:helicase activity; IEA.
KW Helicase.
FT NON_TER 1 1
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2588 MW; C8E13B3B1AD353E3 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 3.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRRRK 6
Db 4 RRRPKK 9

RESULT 28
Q9PRZ3 ONCMY
ID Q9PRZ3 ONCMY PRELIMINARY; PRT; 21 AA.
AC Q9PRZ3
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Neuropeptide-gamma (NP-gamma) (Tachykinin homolog).
OS Onchorynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
ON NCBI_TaxID=8022;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=94056890; PubMed=7694488;
RA Jensen J., Olson K.R., Conlon J.M.;
RT "Primary structures and effects on gastrointestinal motility of
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RT tachykinins from the rainbow trout.";

RL Am. J. Physiol. 265:R804-R810(1993).

DR GO; GO:0005102; P:receptor binding; IEA.

DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.

DR GO; GO:0007268; P:synaptic transmission; IEA.

DR GO; GO:0007217; P:tachykinin signaling pathway; IEA.

DR InterPro; IPR002040; TachyNeurokinin.

DR Pfam; PF02202; Tachykinin_1.

DR PROSITE; PS00267; TACHYKININ; UNKNOWN_1.

KW Neuropeptide; Tachykinin.

SQ SEQUENCE 21 AA; 2385 MW; 080CAC6E36997A29 CRC64;

Query Match 66.7%; Score 20; DB 2; Length 21;

Best Local Similarity 80.0%; Pred. No. 3.6e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 5

Db 9 RKRRK 13

RESULT 29

Q70Y78 9LAMI

ID Q70Y78 9LAMI PRELIMINARY; PRT; 10 AA.

AC Q70Y78;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Ribosomal protein (Fragment).

GN Name=rpel6;

OS Plectranthus parishii.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Lamiales; Lamiaceae; Nepetoideae; Plectranthus.

OX NCBI_TaxID=204190;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;

RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,

RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;

RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)

RT based on three plastid DNA regions.";

RL Mol. Phylogenet. Evol. 31:277-299(2004).

DR EMBL; AJ505390; CAD45510.1; -; Genomic DNA.

DR GO; GO:0003735; P:structural constituent of ribosome; IEA.

KW Ribosomal protein.

FT NON_TER 1

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1299 MW; 87C8C86723241411 CRC64;

Query Match 63.3%; Score 19; DB 2; Length 10;

Best Local Similarity 80.0%; Pred. No. 2.6e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 5

Db 2 RTRRK 6

RESULT 30

Q70Y85 9LAMI

ID Q70Y85 9LAMI PRELIMINARY; PRT; 11 AA.

AC Q70Y85;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Ribosomal protein (Fragment).

GN Name=rpel6;

OS Platostoma rubrum.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC lamids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Platostoma.

OX NCBI_TaxID=204176;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;

RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,

RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;

RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)

RT based on three plastid DNA regions.";

RL Mol. Phylogenet. Evol. 31:277-299(2004).

DR EMBL; AJ505373; CAD45494.1; -; Genomic DNA.

DR GO; GO:0003735; P:structural constituent of ribosome; IEA.

KW Ribosomal protein.

FT NON_TER 1

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1430 MW; 7397DC9867232414 CRC64;

Query Match 63.3%; Score 19; DB 2; Length 11;

Best Local Similarity 80.0%; Pred. No. 2.9e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RKRRK 5

Db 2 RTRRK 6

Search completed: April 13, 2006, 08:49:02

Job time : 232 secs

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